

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: * June 11, 2003, 17:57:02 ; Search time 2186 Seconds

(without alignments)
10592.969 Million cell updates/sec

Title: US-09-308-397-1

Perfect score: 921

Sequence: 1 atgactaaacagccttttt.....tagcacttttagaaaaatag 921

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_NA_Main:*

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Forman
09/308397
Seq IDs 172 w/
Interf.

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- 45: /cgn2_6/ptodata/2/pna/US6001 COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	921	100.0	921	17	US-09-308-397-1 Sequence 1, Appli
2	913	99.1	921	22	US-09-583-110-1251 Sequence 1251, Ap
3	913	99.1	921	29	US-09-752-069A-30 Sequence 30, Appl
4	913	99.1	921	61	US-60-174-089-30 Sequence 30, Appl
5	913	99.1	924	15	US-09-107-433-794 Sequence 794, App
6	913	99.1	13702	41	US-10-158-844-7 Sequence 7, Appli
C 6	913	99.1	13706	46	US-60-029-960-61 Sequence 61, Appl
C 7	913	99.1	13706	41	PCT-US02-03987-9482 Sequence 9482, Ap
8	911.4	99.0	921	31	US-09-815-242-9482 Sequence 9482, Ap
9	911.4	99.0	921	39	US-10-073-851-9482 Sequence 43, Appl
10	911.4	99.0	3580	1	PCT-US97-32578-43 Sequence 555, App
11	911.4	99.0	9753	50	US-60-068-175-555 Sequence 256, App
12	908.4	98.6	945	29	US-09-752-069A-256 Sequence 494, App
13	891.6	96.8	5963	50	US-60-061-998-494 Sequence 5, Appli
14	529.4	57.5	547	17	US-09-308-397-5 Sequence 8, Appli
15	523.2	56.8	1196	1	PCT-US97-07950-8 Sequence 78, Appl
16	523.2	56.8	1199	12	US-08-832-030-78 Sequence 81, Appl
C 17	523.2	56.8	1209	16	US-09-297-451-81 Sequence 81, Appl
18	523.2	56.8	1209	16	US-09-297-451A-81 Sequence 157, App
C 19	523.2	56.8	1209	16	US-08-832-030-157 Sequence 42057, A
20	402	43.6	636	12	US-08-832-030-157 Sequence 42057, A
21	388.8	42.2	927	80	US-60-360-033-42057 Sequence 42057, A

22 366 39.7 450 17 US-09-308-397-3 Sequence 3, Appli
23 350.8 38.1 948 15 US-09-134-000-1582 Sequence 1582, Ap
24 344.4 37.4 942 1 PCT-US02-03987-6823 Sequence 6823, Ap
25 344.4 37.4 942 31 US-09-815-243-6823 Sequence 6823, Ap
26 344.4 37.4 942 39 US-10-072-851-6823 Sequence 6823, Ap
27 340.4 37.0 3656 14 US-09-070-927-577 Sequence 577, App
28 340.4 37.0 3656 14 US-09-070-927A-577 Sequence 577, App
29 316.8 34.4 2969 49 US-60-050-444-527 Sequence 527, App
30 316.8 34.4 2969 50 US-60-068-186-533 Sequence 533, App
31 315.2 34.2 987 15 US-09-107-532-3319 Sequence 3319, Ap
32 315.2 34.2 987 15 US-09-107-532A-3319 Sequence 3319, Ap
33 301 32.7 3627 48 US-60-045-649-929 Sequence 929, App
34 301 32.7 3627 48 US-60-046-653-916 Sequence 916, App
35 301 32.7 3627 50 US-60-068-217-803 Sequence 803, App
36 204 22.1 950 36 US-09-974-300-1086 Sequence 1086, Ap
37 204 22.1 950 36 US-09-974-300-1086 Sequence 1086, Ap
38 198.2 21.5 1002 21 US-09-543-681A-3811 Sequence 3811, Ap
39 196.4 21.3 939 1 PCT-US02-03987-6878 Sequence 6878, Ap
40 196.4 21.3 939 31 US-09-815-243-6878 Sequence 6878, Ap
41 196.4 21.3 939 39 US-10-072-851-6878 Sequence 6878, Ap
42 196.4 21.3 1830121 8 US-08-426-787-1 Sequence 1, Appli
43 196.4 21.3 1830121 22 US-09-557-884-1 Sequence 1, Appli
44 196.4 21.3 1830121 25 US-09-643-990A-1 Sequence 1, Appli
45 196.6 20.3 1198 27 US-09-680-598A-74 Sequence 74, Appli

ALIGNMENTS

RESULT 1
US-09-308-397-1
; Sequence 1, Application US/09308397
; GENERAL INFORMATION:
; APPLICANT: Gentry, Daniel R.
; APPLICANT: Lonsdale, John T.
; APPLICANT: Payne, David J.
; APPLICANT: Pearson, Stewart C.
; APPLICANT: Van Aller, Glenn
; TITLE OF INVENTION: Novel Fabb
; FILE REFERENCE: P50593
; CURRENT APPLICATION NUMBER: US/09/308,397
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: US 60/031,160
; EARLIER FILING DATE: 1996-11-18
; EARLIER APPLICATION NUMBER: PCT/US97/20992
; EARLIER FILING DATE: 1997-11-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-308-397-1
Query Match 100.0%; Score 921; DB 17; Length 921;
Best Local Similarity 100.0%; Pred. No. 2.4e-271;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGACTAAACAGCCTTTTATTTGCTGTCAGAGTGCCCGAGTATCTAGGATGGACGG 60
Db 1 ATGACTAAACAGCCTTTTATTTGCTGTCAGAGTGCCCGAGTATCTAGGATGGACGG 60
Qy 61 GATTTCATGATCAGTATCCGATGTCACAAAGAACGATTGATCGAGGATCAGGTGCTC 120
Db 61 GATTTCATGATCAGTATCCGATGTCACAAAGAACGATTGATCGAGGATCAGGTGCTC 120
Qy 121 GGTTCATGATTTAGTTCATCTCATCGATACGGAAGACAAACTCAATCAGACCCGCTAT 180
Db 121 GGTTCATGATTTAGTTCATCTCATCGATACGGAAGACAAACTCAATCAGACCCGCTAT 180
Qy 181 ACGCAACACGCCATCTTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAGGC 240
Db 181 ACGCAACACGCCATCTTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAGGC 240

Qy 241 TATCAGCCTGATATGCTTCTGCTGTTTCTCTTTCGAGAACTACTCTGCTTGGTGGCAGC 300
Db 241 TATCAGCCTGATATGCTTCTGCTGTTTCTCTTTCGAGAACTACTCTGCTTGGTGGCAGC 300
Qy 301 GCGCCTTGGATTTTGAAGATGCGGTTGCTTGGTAGCTAAGCGTGGAGCCTATATGGAA 360
Db 301 GCGCCTTGGATTTTGAAGATGCGGTTGCTTGGTAGCTAAGCGTGGAGCCTATATGGAA 360
Qy 361 GAACGGCTCTCTGCTGCTCTGCGCAAGATGCTAGCAGTTCTCAATAGCCAGTAGAGTC 420
Db 361 GAACGGCTCTCTGCTGCTCTGCGCAAGATGCTAGCAGTTCTCAATAGCCAGTAGAGTC 420
Qy 421 ATTGAAGAAGCCTCTCAAAAGCTTCTGAACCTTGGAGTGGTTACTCCAGCAACTATAAC 480
Db 421 ATTGAAGAAGCCTCTCAAAAGCTTCTGAACCTTGGAGTGGTTACTCCAGCAACTATAAC 480
Qy 481 ACACCTGCAAAATCGTCATTTGCTGGAGAAAGTGGTTGCAGTTGATCGAGCGTTGAACCT 540
Db 481 ACACCTGCAAAATCGTCATTTGCTGGAGAAAGTGGTTGCAGTTGATCGAGCGTTGAACCT 540
Qy 541 TTGCAAGAAGCAGGTGCAAAAGCTTGAATTCCTTAAAGGTGTCAGGTCCCTTTCAACAC 600
Db 541 TTGCAAGAAGCAGGTGCAAAAGCTTGAATTCCTTAAAGGTGTCAGGTCCCTTTCAACAC 600
Qy 601 GCTCTCTTGGCTGCTAGCCAGAACTAGCTGAAACTCTAGCTCAGTAAAGTTTTC 660
Db 601 GCTCTCTTGGCTGCTAGCCAGAACTAGCTGAAACTCTAGCTCAGTAAAGTTTTC 660
Qy 661 GATTTTACTTCCCTAGTCGCAATACAGAACTGCTGTGATGCAAAAGAGGACATT 720
Db 661 GATTTTACTTCCCTAGTCGCAATACAGAACTGCTGTGATGCAAAAGAGGACATT 720
Qy 721 GCTCAGCTTTCAGCGCTCAGGTCAAGGAAACCCGTTCTTCTATGAAAGTATTGGGTC 780
Db 721 GCTCAGCTTTCAGCGCTCAGGTCAAGGAAACCCGTTCTTCTATGAAAGTATTGGGTC 780
Qy 781 ATGCAAGAAGCAGCATTAAGCACTTTATCGAATTGCGACCGGGAAGCTTCTTCAGGT 840
Db 781 ATGCAAGAAGCAGCATTAAGCACTTTATCGAATTGCGACCGGGAAGCTTCTTCAGGT 840
Qy 841 TTTGTTAAAAAATTGATCAAACTGCTCAGTTAGCTCATGTGGAAGATCAAGCGAGTTTA 900
Db 841 TTTGTTAAAAAATTGATCAAACTGCTCAGTTAGCTCATGTGGAAGATCAAGCGAGTTTA 900
Qy 901 GTAGCACTTTTAGAAATAAG 921
Db 901 GTAGCACTTTTAGAAATAAG 921

RESULT 2
US-09-583-110-1251
; Sequence 1251, Application US/09583110
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 1251
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-1251

Query Match		99.1%	Score 913;	DB 22;	Length 921;
Best Local Similarity 99.5%;		Pred. No. 7e-269;			
Matches 916;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;	
Qy	1	ATGACTAAACAGCGCTTTTATTTGCTGGTCAAGTGCCCAAGTATCTAGGATGGACGG	60		
Db	1	ATGACTAAACAGCGCTTTTATTTGCTGGTCAAGTGCCCAAGTATCTAGGATGGACGG	60		
Qy	61	GATTTCTATGATCAGTATCCGATTGTCMAAGAAACGATTTGATCAGCGAGTCAAGTGCT	120		
Db	61	GATTTCTATGATCAGTATCCGATTGTCMAAGAAACGATTTGATCAGCGAGTCAAGTGCT	120		
Qy	121	GGTTATGATTTACGTTATCTCATCGATACGGAAGAACAACTCAATCAGACCCGCTAT	180		
Db	121	GGTTATGATTTACGTTATCTCATCGATACGGAAGAACAACTCAATCAGACCCGCTAT	180		
Qy	181	ACGCAACCGACCATCTAGCGACTTCGGTTGCTATCTACCGTTTATTCGAAGAAAGGGC	240		
Db	181	ACGCAACCGACCATCTAGCGACTTCGGTTGCTATCTACCGTTTATTCGAAGAAAGGGC	240		
Qy	241	TATCAGCGCTGATATGTTGCTGGTTTGTCTCTGGAGAATACTCTGCCCTGGTGGCAAGC	300		
Db	241	TATCAGCGCTGATATGTTGCTGGTTTGTCTCTGGAGAATACTCTGCCCTGGTGGCAAGC	300		
Qy	301	GGCGCTTGATTTTGAAGATGCGGTTGCCCTTGGTAGCTAAGCGTGAGCCCTATATGGAA	360		
Db	301	GGCGCTTGATTTTGAAGATGCGGTTGCCCTTGGTAGCTAAGCGTGAGCCCTATATGGAA	360		
Qy	361	GAAGCGGCTCCTGCTGACTCTGGCAAGATGTTAGCAGTTCTCAATACGCCAGTAGAGGTC	420		
Db	361	GAAGCGGCTCCTGCTGACTCTGGCAAGATGTTAGCAGTTCTCAATACGCCAGTAGAGGTC	420		
Qy	421	ATTGAAGAGCGCTGTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCAGGCCAATATTAAC	480		
Db	421	ATTGAAGAGCGCTGTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCAGGCCAATATTAAC	480		
Qy	481	ACACTGCACAAATCGTCAATTCGTGGAGAGTGGTTGCAGTTGATCGAGCGGTTGAACCT	540		
Db	481	ACACTGCACAAATCGTCAATTCGTGGAGAGTGGTTGCAGTTGATCGAGCGGTTGAACCT	540		
Qy	541	TTGAAGAGAGCGTGCCAAACGCTTGATTCCTCTTAAGTGTGAGTCCCTTTACACC	600		
Db	541	TTGAAGAGAGCGTGCCAAACGCTTGATTCCTCTTAAGTGTGAGTCCCTTTACACC	600		
Qy	601	GCTCTCTTGAGCCTGTAGCCAGAAACTAGCTGAACTCTAGCTCAGTAAGTTTTCATCA	660		
Db	601	GCTCTCTTGAGCCTGTAGCCAGAAACTAGCTGAACTCTAGCTCAGTAAGTTTTCATCA	660		
Qy	661	GATTTTACTTGTCCCTAGTCCGCAATACAGAGCTGCTGTGATGCAAAAAGAGACATT	720		
Db	661	GATTTTACTTGTCCCTAGTCCGCAATACAGAGCTGCTGTGATGCAAAAAGAGACATT	720		
Qy	721	GCTCAGCTCTTGAGCGTCAAGTCAAGGAAACCGTTTCGTTCTATGAAAGTATTTGGGTC	780		
Db	721	GCTCAGCTCTTGAGCGTCAAGTCAAGGAAACCGTTTCGTTCTATGAAAGTATTTGGGTC	780		
Qy	781	ATGCAAGAGCAGCGATTAAGCAATTTATCAGATTTGACCGGGGAAAGTCTTGTCAAGT	840		
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Qy	841	TTTGTATAAAAAATGATCAAACTGCTCAGTTAGCTCATGTGGAAGATCAAGCGAGTTTA	900		
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Qy	901	GTAGCACTTTTAAAAAATAG	921		
Db	901	GTAGCACTTTTAAAAAATAG	921		

RESULT 3
US-09-752-069A-30
; Sequence 30, Application US/09752069A
; GENERAL INFORMATION:

/ APPLICANT: Dougherty, Thomas J.
 / APPLICANT: Pucci, Michael J.
 / APPLICANT: Dougherty, Brian A.
 / APPLICANT: Davison, Daniel B.
 / APPLICANT: Bruccoleri, Robert E.
 / APPLICANT: Thanassi, Jane A.
 / APPLICANT: Farmer II, Bennett T.
 / TITLE OF INVENTION: NOVEL BACTERIAL GENES AND PROTEINS THAT ARE ESSENTIAL
 / TITLE OF INVENTION: FOR CELL VIABILITY AND THEIR USES
 / FILE REFERENCE: D0001NP
 / CURRENT APPLICATION NUMBER: US/09/752,069A
 / CURRENT FILING DATE: 2000-12-29
 / PRIOR APPLICATION NUMBER: 60/174,089
 / PRIOR FILING DATE: 1999-12-30
 / NUMBER OF SEQ ID NOS: 338
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 30
 / LENGTH: 921
 / TYPE: DNA
 / ORGANISM: Streptococcus pneumoniae
 / US-09-752-069A-30

Query Match	99.1%	Score 913	DB 29	Length 921
Best Local Similarity	99.5%	Pred. No. 7e-269		
Matches 916	Conservative 0	Mismatches 5	Indels 0	Gaps 0
QY	1	ATGACTAAACAGCGCTTTTATTTGCTGGTCAAGGTGCCAGTATCTAGGATGGGACGG	60	
DB	1	ATGACTAAACAGCGCTTTTATTTGCTGGTCAAGGTGCCAGTATCTAGGATGGGACGG	60	
QY	61	GATTTCATGATCAGTATCCGATTGTCAAAGAACGATTGATCGAGCGATCAGGTGCTC	120	
DB	61	GATTTCATGATCAGTATCCGATTGTAAAGAACGATTGATCGAGCGATCAGGTGCTC	120	
QY	121	GGTTATGATTTACGTTATCTCATCGATACGGAAGACACAACTCAATCAGACCCGCTAT	180	
DB	121	GGTTATGATTTGCGTTATCTCATCGATACGGAAGAGCAAACTCAATCAGACCCGCTAT	180	
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DB	181	ACGCAACAGCAATTCAGCACTTCGTTTGCTATCTACCGTTTATTCGAAGAAAAGGGC	240	
QY	241	TATCAGGCTGATATGGTTGCTGGTTTCTCTCTGGAGAACTACTCTGCTTGGTGGCAAGC	300	
DB	241	TATCAGGCTGATATGGTTGCTGGTTTCTCTCTGGAGAACTACTCTGCTTGGTGGCAAGC	300	
QY	301	GGCGCTTTGGAATTTTGAAGATGCGGTTGCTTGGTAGCTAAGCGTGGAGGCTATATGGAA	360	
DB	301	GGCGCTTTGGAATTTTGAAGATGCGGTTGCTTGGTAGCTAAGCGTGGAGGCTATATGGAA	360	
QY	361	GAACGGCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGTTC	420	
DB	361	GAACGGCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGTTC	420	
QY	421	ATTGAAGAAGCTGCTCAAAAAGCTTCGAATCTGGAGTGGTTACTCCAGGCCAATATAAC	480	
DB	421	ATTGAAGAAGCTGCTCAAAAAGCTTCGAATCTGGAGTGGTTACTCCAGGCCAATATAAC	480	
QY	481	ACACCTGCACAAATCGTCAATTTGCGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACCT	540	
DB	481	ACACCTGCACAAATCGTCAATTTGCGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACCT	540	
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DB	541	TTGCAAGAAGCAGGTGCAAAACGGTTGATTCCTCTTAAAGGTGTCAGTCCCTTTACACC	600	
QY	601	GCTCTCCTTGAGCCTGCTAGCCAGAACTAGCTGAAACTCTAGCTCAGGTAAAGTTTTCAC	660	
DB	601	GCTCTCCTTGAGCCTGCTAGCCAGAACTAGCTGAAACTCTAGCTCAGGTAAAGTTTTCAC	660	
QY	661	GATTTTACTTGTGCCCTAGTCGGCAATACAGAGCTGCTGTGATGCAAAAAGAGGACATT	720	
DB	661	GATTTTACTTGTGCCCTAGTCGGCAATACAGAGCTGCTGTGATGCAAAAAGAGGACATT	720	

QY 721 GCTCAGCTTTGACGCGTCAGGTCAAGGAACCCGTTCTTCTATGAAAGTATTGGGGTC 780
Db 721 GCTCAGCTTTGACGCGTCAGGTCAAGGAACCCGTTCTTCTATGAAAGTATTGGGGTC 780
QY 781 ATGCAAGAAGCAGGATCAAGCAACTTATCGAGATTGACCGGGGAAAGTCTTGTCAAGT 840
Db 781 ATGCAAGAAGCAGGATCAAGCAACTTATCGAGATTGACCGGGGAAAGTCTTGTCAAGT 840
QY 841 TTTGTTAAAAAATGATCAAACTGCTCACTAGCTCATGTGGAAGATCAAGCGAGTTTA 900
Db 841 TTTGTTAAAAAATGATCAAACTGCTCACTAGCTCATGTGGAAGATCAAGCGAGTTTA 900
QY 901 GTAGCACTTTTAGAAAAATAG 921
Db 901 GTAGCACTTTTAGAAAAATAG 921

RESULT 4
US-60-174-089-30
; Sequence 30, Application US/60174089
; GENERAL INFORMATION:
; APPLICANT: Dougherty, Thomas J.
; APPLICANT: Pucci, Michael J.
; APPLICANT: Dougherty, Brian A.
; APPLICANT: Davidson, Daniel B.
; TITLE OF INVENTION: NOVEL BACTERIAL GENES AND PROTEINS THAT ARE ESSENTIAL
; FILE REFERENCE: 30436.4USP1
; CURRENT APPLICATION NUMBER: US/60/174.089
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-60-174-089-30

Query Match 99.1%; Score 913; DB 61; Length 921;
Best Local Similarity 99.5%; Pred. No. 7e-269;
Matches 916; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGACTAAACAGCGCTTTTATTGCTGGTCAAGGTGCCAGTATCTAGGGATGGGACGG 60
Db 1 ATGACTAAACAGCGCTTTTATTGCTGGTCAAGGTGCCAGTATCTAGGGATGGGACGG 60
QY 61 GATTCTATGATCAGTATCCGATTGTCAGGAAGACGATTCATCGAGCGAGTCAGGTGCTC 120
Db 61 GATTCTATGATCAGTATCCGATTGTCAGGAAGACGATTCATCGAGCGAGTCAGGTGCTC 120
QY 121 GGTATGATTTACGTTATCTCATCGATACGGAAGACAACTCAATCAGACCCGCTAT 180
Db 121 GGTATGATTTACGTTATCTCATCGATACGGAAGACAACTCAATCAGACCCGCTAT 180
QY 181 ACGCAACAGCGCTTTAGGACGTTGGTGGTCTATCTACCGTTTATTGCAAGAAAGGCG 240
Db 181 ACGCAACAGCGCTTTAGGACGTTGGTGGTCTATCTACCGTTTATTGCAAGAAAGGCG 240
QY 241 TATCAGCGCTGATGTTGTTGCTCTCTTTGGGAATPACTCTGCTTGGTGGCAAGC 300
Db 241 TATCAGCGCTGATGTTGTTGCTCTCTTTGGGAATPACTCTGCTTGGTGGCAAGC 300
QY 301 GCGCGCTTGATTTTGAAGATGGGTTGCTTGGTAGCTAAGCGTGGAGCTATATGGAA 360
Db 301 GCGCGCTTGATTTTGAAGATGGGTTGCTTGGTAGCTAAGCGTGGAGCTATATGGAA 360
QY 361 GAAGCGCTCTGCTGACTCTGGCAAGATGTTAGCAGTCTCAATACGCCAGTAGAGGTC 420
Db 361 GAAGCGCTCTGCTGACTCTGGCAAGATGTTAGCAGTCTCAATACGCCAGTAGAGGTC 420
QY 421 ATTGAAGAAGCGCTTCAAAAGCTTCTGAACCTTGGAGTGGTCTACTCAGCAACTATAC 480

Db 421 ATTGAAGAAGCGCTTCAAAAGCTTCTGAACCTTGGAGTGGTCTACTCCAGCAACTATAAC 480
QY 481 ACACCTGCACAAATCGTCAATTCCTGGAGAGTGGTTCAGTTCATGATCGAGCGGTTGAACTT 540
Db 481 ACACCTGCACAAATCGTCAATTCCTGGAGAGTGGTTCAGTTCATGATCGAGCGGTTGAACTT 540
QY 541 TTGCAAGAAGCAGGTGCGCAACCGTTGATTCCTCTTAAGGTGTCAGGTCCCTTTTCACACC 600
Db 541 TTGCAAGAAGCAGGTGCGCAACCGTTGATTCCTCTTAAGGTGTCAGGTCCCTTTTCACACC 600
QY 601 GCTCTCCTTTGAGCGCTTAGCCAGAACTAGCTGAAACTCTAGCTCAGGTAAAGTTTTCAC 660
Db 601 GCTCTCCTTTGAGCGCTTAGCCAGAACTAGCTGAAACTCTAGCTCAGGTAAAGTTTTCAC 660
QY 661 GATTTTACTTGTCCCTTAGTCGGCAATACAGAACTGCTGTGATGCAAAAAAGAGACATT 720
Db 661 GATTTTACTTGTCCCTTAGTCGGCAATACAGAACTGCTGTGATGCAAAAAAGAGACATT 720
QY 721 GCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTCTTCTATGAAAGTATTGGGGTC 780
Db 721 GCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTCTTCTATGAAAGTATTGGGGTC 780
QY 781 ATGCAAGAAGCAGGATCAAGCAACTTTATCGAGATTGACCGGGGAAAGTCTTGTCAAGT 840
Db 781 ATGCAAGAAGCAGGATCAAGCAACTTTATCGAGATTGACCGGGGAAAGTCTTGTCAAGT 840
QY 841 TTTGTTAAAAAATGATCAAACTGCTCACTAGCTCATGTGGAAGATCAAGCGAGTTTA 900
Db 841 TTTGTTAAAAAATGATCAAACTGCTCACTAGCTCATGTGGAAGATCAAGCGAGTTTA 900
QY 901 GTAGCACTTTTAGAAAAATAG 921
Db 901 GTAGCACTTTTAGAAAAATAG 921

RESULT 5
US-09-107-433-794
; Sequence 794, Application US/09107433
; GENERAL INFORMATION:
; APPLICANT: Lynn A. Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107.433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 794:
; SEQUENCE CHARACTERISTICS:


```

; LENGTH: 924 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...924
; SEQUENCE DESCRIPTION: SEQ ID NO: 794:
US-09-107-433-794

Query Match          99.1%; Score 913; DB 15; Length 924;
Best Local Similarity 99.5%; Pred. No. 7e-269;
Matches 916; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGACTAAACAGAGCTTTTATTTGCTGGTCAAGGTGCCAGATCTTAGGGATGGACGG 60
DB 4 ATGACTAAACAGAGCTTTTATTTGCTGGTCAAGGTGCCAGATCTTAGGGATGGACGG 63
QY 61 GATTTCTATGATCAGTATCCGATTCGAAAGAACGATTCGAGCGAGTCAGGTGCTC 120
DB 64 GATTTCTATGATCAGTATCCGATTCGAAAGAACGATTCGAGCGAGTCAGGTGCTC 123
QY 121 GGTATGATTTACGTTATCTCATCGATACGGAAGAACAACTCAATCAGACCGCTAT 180
DB 124 GGTATGATTTGCGTTATCTCATCGATACGGAAGAACAACTCAATCAGACCGCTAT 183
QY 181 ACGCAACAGAGCTTTAGGAGCTTCGGTGGTCTATACCGTTTATTTGCAAGAAAGGCG 240
DB 184 ACGCAACAGAGCTTTAGGAGCTTCGGTGGTCTATACCGTTTATTTGCAAGAAAGGCG 243
QY 241 TATCAGCTGATATGGTGTGCTGTTGCTCTCGAGAACTCTGCTTTGGTGGCAAGC 300
DB 244 TATCAGCTGATATGGTGTGCTGTTGCTCTCGAGAACTCTGCTTTGGTGGCAAGC 303
QY 301 GCGCGCTTGGATTTGAAGATCGCGTTGCTTGTAGTAAAGCGTGGAGCTTATGGAA 360
DB 304 GCGCGCTTGGATTTGAAGATCGCGTTGCTTGTAGTAAAGCGTGGAGCTTATGGAA 363
QY 361 GAAGCGGCTCGTCTGACTCTGCAAGATGTAGCACTTCTCAATAGCCAGTAGAGTC 420
DB 364 GAAGCGGCTCGTCTGACTCTGCAAGATGTAGCACTTCTCAATAGCCAGTAGAGTC 423
QY 421 ATTGAAGAGCTCTCAAAAGCTTCTGAATTTGGAGTGTCTACTCCAGCAACTATAAC 480
DB 424 ATTGAAGAGCTCTCAAAAGCTTCTGAATTTGGAGTGTCTACTCCAGCAACTATAAC 483
QY 481 ACACCTGCACAAATCGTCNTGCTGGAGAGTGGTTGCAGTTGATCGAGCGTTGACCTT 540
DB 484 ACACCTGCACAAATCGTCNTGCTGGAGAGTGGTTGCAGTTGATCGAGCGTTGACCTT 543
QY 541 TTGCAAGAGCAGGTGCCAAACGCTTGAATTCCTTAAAGTGTGAGTCCCTTTTCACAC 600
DB 544 TTGCAAGAGCAGGTGCCAAACGCTTGAATTCCTTAAAGTGTGAGTCCCTTTTCACAC 603
QY 601 GCTCTCTTGGCTGTAGTCAGCAAACTAGCTGAAACTCTAGTCAAGTAAGTTTTC 660
DB 604 GCTCTCTTGGCTGTAGTCAGCAAACTAGCTGAAACTCTAGTCAAGTAAGTTTTC 663
QY 661 GATTTTACTTGTCCCTAGTCGGCAATACAGAACTGCTGTGATGCAAAAGAGGACATT 720
DB 664 GATTTTACTTGTCCCTAGTCGGCAATACAGAACTGCTGTGATGCAAAAGAGGACATT 723
QY 721 GCTCAGCTCTTGAAGCGTCAGGTCAAGAACCCGTTTCGTTTCTATGAAAGTATGGGGTC 780
DB 724 GCTCAGCTCTTGAAGCGTCAGGTCAAGAACCCGTTTCGTTTCTATGAAAGTATGGGGTC 783
QY 781 ATGCAAGAGCAGGCAATGAAGCAATTTATCGAGATTGGACCGGGGAAGCTTGTGAGGT 840
DB 784 ATGCAAGAGCAGGCAATGAAGCAATTTATCGAGATTGGACCGGGGAAGCTTGTGAGGT 843
QY 841 TTTGTTAAAAAATTGATCAAACTGCTCAGTCTAGTCTATGTTGAAAGATCAAGCGAGTTTA 900
DB 844 TTTGTTAAAAAATTGATCAAACTGCTCAGTCTAGTCTATGTTGAAAGATCAAGCGAGTTTA 903
QY 901 GTAGCACTTTTAGAAAAATAG 921
DB 904 GTAGCACTTTTAGAAAAATAG 924

RESULT 6
US-10-158-844-7/c
; Sequence 7, Application US/10158844
; GENERAL INFORMATION:
; APPLICANT: Kunsch et al.
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; COMPUTER: Dell Latitude Pentium 3
; OPERATING SYSTEM: Windows 98
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/158,844
; FILING DATE: 03-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/961,527
; FILING DATE: 1997-10-30
; APPLICATION NUMBER: US 60/029,960
; FILING DATE: 1996-10-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Hyman, Mark J.
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB340P:DI
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-158-844-7

Query Match          99.1%; Score 913; DB 41; Length 19702;
Best Local Similarity 99.5%; Pred. No. 2.9e-268;
Matches 916; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGACTAAACAGAGCTTTTATTTGCTGGTCAAGGTGCCAGATCTTAGGGATGGACGG 60
DB 17149 ATGACTAAACAGAGCTTTTATTTGCTGGTCAAGGTGCCAGATCTTAGGGATGGACGG 17090
QY 61 GATTTCTATGATCAGTATCCGATTCGAAAGAACGATTCGAGCGAGTCAGGTGCTC 120
DB 17089 GATTTCTATGATCAGTATCCGATTCGAAAGAACGATTCGAGCGAGTCAGGTGCTC 17030
QY 121 GGTATGATTTACGTTATCTCATCGATACGGAAGAACAACTCAATCAGACCGCTAT 180
DB 17029 GGTATGATTTACGTTATCTCATCGATACGGAAGAACAACTCAATCAGACCGCTAT 16970
QY 181 ACGCAACAGAGCTTTAGGAGCTTCGGTGGTCTATCTACCGTTTATTTGCAAGAAAGGCG 240
DB 16969 ACGCAACAGAGCTTTAGGAGCTTCGGTGGTCTATCTACCGTTTATTTGCAAGAAAGGCG 16910
QY 241 TATCAGCTGATATGGTGTGCTGTTGCTCTCTTGAGAAATACTCTGCTTGGTGGCAAGC 300
```

Db 16909 TATCAGCCTGATATGGTGTGCTGTTGCTCTTTGGAGATATCTGCTCTGGTGGCAAGT 16850
Qy 301 GGGCGCTTGGATTGTAAGATGCGGTGCTGCTGGTAGCTAAGCGTGGAGCCCTATATGGAA 360
Db 16849 GGGCGCTTGGATTGTAAGATGCGGTGCTGCTGGTAGCTAAGCGTGGAGCCCTATATGGAA 16790
Qy 361 GRAGCGCTCTGCTGACTCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 420
Db 16789 GAAGCGCTCTGCTGACTCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 16730
Qy 421 ATTGAAGAGCGCTCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 480
Db 16729 ATTGAAGAGCGCTCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 16670
Qy 481 ACACCTGCAAAATGCTGCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 540
Db 16669 ACACCTGCAAAATGCTGCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 16610
Qy 541 TTGCAAGAGCGCTGCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 600
Db 16609 TTGCAAGAGCGCTGCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 16550
Qy 601 GCTCTCTGAGCGCTGCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 660
Db 16549 GCTCTCTGAGCGCTGCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 16490
Qy 661 GATTTTACTTGTCCCTGAGCGCTGCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 720
Db 16489 GATTTTACTTGTCCCTGAGCGCTGCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 16430
Qy 721 GCTCAGCTCTGAGCGCTGCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 780
Db 16429 GCTCAGCTCTGAGCGCTGCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 16370
Qy 781 ATGCAAGAGCGCTGCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 840
Db 16369 ATGCAAGAGCGCTGCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 16310
Qy 841 TTTGTTAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTA 900
Db 16309 TTTGTTAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTA 16250
Qy 901 GTAGCACTTTAGAAAAATAG 921
Db 16249 GTAGCACTTTAGAAAAATAG 16229

RESULT 7

US-60-029-960-61/c
; Sequence 61, Application US/60029960
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 1649
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/029,960
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19706 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-60-029-960-61

Query Match 99.1%; Score 913; DB 46; Length 19706;
Best Local Similarity 99.5%; Pred. No. 2.9e-268;
Matches 916; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGACTAAACACAGCCTTTTATTTGCTGCTCAAGGTGCCAGATCTAGGGATGGACGG 60
Db 17155 ATGACTAAACACAGCCTTTTATTTGCTGCTCAAGGTGCCAGATCTAGGGATGGACGG 17096
Qy 61 GATTTCTATGATCAGTATCCGATTGTCAAAGAACGATTGATCGAGCGAGTCAAGTCTC 120
Db 17095 GATTTCTATGATCAGTATCCGATTGTCAAAGAACGATTGATCGAGCGAGTCAAGTCTC 17036
Qy 121 GGTATGATTTAGTATCTCATCGATACGGAAGAGACAACTCAATCAGACCCGCTAT 180
Db 17035 GGTATGATTTAGTATCTCATCGATACGGAAGAGACAACTCAATCAGACCCGCTAT 16976
Qy 181 ACACCAACAGCCATCTCAGCGACTTCGGTTGCTATCTACCGTTTATTCGAAAGAAAGGGC 240
Db 16975 ACACCAACAGCCATCTCAGCGACTTCGGTTGCTATCTACCGTTTATTCGAAAGAAAGGGC 16916
Qy 241 TATCAGCCTGATATGGTGTGCTGCTCTCTTTGGAGATACCTCTGCTTGGTGGCAAGC 300
Db 16915 TATCAGCCTGATATGGTGTGCTGCTCTCTTTGGAGATACCTCTGCTTGGTGGCAAGT 16856
Qy 301 GGGCCCTTGGATTTTGAAGATGCGGTTCCTTGGTAGCTAAGCGTGGAGCTATATGGAA 360
Db 16855 GGGCCCTTGGATTTTGAAGATGCGGTTCCTTGGTAGCTAAGCGTGGAGCTATATGGAA 16796
Qy 361 GAAGCGCTCTGCTGATCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 420
Db 16795 GAAGCGCTCTGCTGATCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 16736
Qy 421 ATTGAAGAGCGCTGCTCAAAAGCTTCTGAACTTGGAGTGGTACTCCAGCCAACTATAAC 480
Db 16735 ATTGAAGAGCGCTGCTCAAAAGCTTCTGAACTTGGAGTGGTACTCCAGCCAACTATAAC 16676
Qy 481 ACACCTGCAAAATCGTCAATGCTGGAGAGTGGTTCAGTTCGAGCGGTGAACTT 540
Db 16675 ACACCTGCAAAATCGTCAATGCTGGAGAGTGGTTCGAGTTCGAGCGGTGAACTT 16616
Qy 541 TTGCAAGAGCGCTGCTCAAAAGCTTCTGAACTTGGAGTGGTACTCCAGCTTTCACAC 600
Db 16615 TTGCAAGAGCGCTGCTCAAAAGCTTCTGAACTTGGAGTGGTACTCCAGCTTTCACAC 16556
Qy 601 GCTCTCTGAGCGCTGCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 660
Db 16555 GCTCTCTGAGCGCTGCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 16496
Qy 661 GATTTTACTTGTCCCTGAGCGCTGCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 720
Db 16495 GATTTTACTTGTCCCTGAGCGCTGCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 16436
Qy 721 GCTCAGCTCTTGGCGCTGCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 780
Db 16435 GCTCAGCTCTTGGCGCTGCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 16376
Qy 781 ATGCAAGAGCGCTGCTGCAAGATGTTCTCAATAGCGCAGTAGAGTC 840

Db 16375 ATGCAAGAGCAGCATAAACAACTTTATCGAGATTGGACCGGGGAAAGTCTTGTCAAGT 16316
Qy 841 TTTGTTTAAAAAATGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTTA 900
Db 16315 TTTGTTTAAAAAATGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTTA 16256
Qy 901 GTAGCACTTTTAGAAAAAATAG 921
Db 16255 GTAGCACTTTTAGAAAAAATAG 16235

RESULT 8
PCT-US02-03987-9482
; Sequence 9482, Application PC/TUS0203987
; GENERAL INFORMATION:
; APPLICANT: Elittra Pharmaceuticals, Inc.
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C
; FILE REFERENCE: ELITRA.028VPC
; CURRENT APPLICATION NUMBER: PCT/US02/03987
; CURRENT FILING DATE: 2002-02-02
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9482
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(921)
PCT-US02-03987-9482

Query Match 99.0%; Score 911.4; DB 1; Length 921;
Best Local Similarity 99.3%; Pred. No. 2.2e-268;
Matches 915; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 ATGACTAAACAGCGCTTTTATTTGCTGGTCAAGGTGCCAGTATCTAGGATGGGACGG 60
Db 1 ATGACTAAACAGCGCTTTTATTTGCTGGTCAAGGTGCCAGTATCTAGGATGGGACGG 60
Qy 61 GATTTCATGATCATCGATCCGATTGTCAAGAAACGATTGATCGAGCGAGTCAGTGCTC 120
Db 61 GATTTCATGATCATCGATCCGATTGTCAAGAAACGATTGATCGAGCGAGTCAGTGCTC 120
Qy 121 GGTATGATTTACGTTATCTCATCGATACGGAAGACAACTCAATCAGACCCGCTAT 180
Db 121 GGTATGATTTACGTTATCTCATCGATACGGAAGACAACTCAATCAGACCCGCTAT 180
Qy 181 ACGCAACAGCCATCTAGCGACTTCGGTTCCTCTGGAGAACTCTGCTTTATGCAAGAAAGGC 240
Db 181 ACGCAACAGCCATCTAGCGACTTCGGTTCCTCTGGAGAACTCTGCTTTATGCAAGAAAGGC 240
Qy 241 TATCAGCTGATATGGTTGCTGTTCTCTCTGGAGAACTCTGCTTTGTTGGCAAGC 300
Db 241 TATCAGCTGATATGGTTGCTGTTCTCTCTGGAGAACTCTGCTTTGTTGGCAAGC 300
Qy 301 GGCCTTGGATTGTAAGATGCGGTTGCTTGGTGTAGCTAAGCGTGGAGCTTATATGAA 360
Db 301 GGCCTTGGATTGTAAGATGCGGTTGCTTGGTGTAGCTAAGCGTGGAGCTTATATGAA 360
Qy 361 GAACGGCTCTGCTGACTCTGGCAAGATGGTACGCTTCTCAATACGCCAGTAGAGGTC 420
Db 361 GAACGGCTCTGCTGACTCTGGCAAGATGGTACGCTTCTCAATACGCCAGTAGAGGTC 420
Qy 421 ATTGAAGAGCTGTCAAAAGCTTCTGAATTTGGAGTGTACTCCAGCCAACTATAAC 480
Db 421 ATTGAAGAGCTGTCAAAAGCTTCTGAATTTGGAGTGTACTCCAGCCAACTATAAC 480
Qy 481 ACACCTGCACAACTGCTATGCTGGAGAAAGTGGTTGCACTTATCGAGCGGTTGAACTT 540

Db 481 ACACCTGCACAACTGCTATGCTGGAGAAAGTGGTTGCACTTATCGAGCGGTTGAACTT 540
Qy 541 TTGCAAGAGCAGGTCGCAAAAGCTTGTATTCCTCTTAAGGTGTCAAGTCCCTTTACACCC 600
Db 541 TTGCAAGAGCAGGTCGCAAAAGCTTGTATTCCTCTTAAGGTGTCAAGTCCCTTTACACCC 600
Qy 601 GCTCTCCTTGGCTGCTAGCCAGAACTAGCTGAAACTCTAGCTCAGCTAAGTATTTTCA 660
Db 601 GCTCTCCTTGGCTGCTAGCCAGAACTAGCTGAAACTCTAGCTCAGCTAAGTATTTTCA 660
Qy 661 GATTTTACTTGTCCCTAGTCGGCAATACAGAAGCTGTGTGATGATCAAAAAGAGACATT 720
Db 661 GATTTTACTTGTCCCTAGTCGGCAATACAGAAGCTGTGTGATGATCAAAAAGAGACATT 720
Qy 721 GCTCAGCTCTTGACCGCTCAGTCAAGGAACCGTTCCTTCTATGAAAGTATTCGGGTC 780
Db 721 GCTCAGCTCTTGACCGCTCAGTCAAGGAACCGTTCCTTCTATGAAAGTATTCGGGTC 780
Qy 781 ATGCAAGAGCAGGTCATGAAGCACTTTATCGAGATTGACCGGGGAAAGTCTTGTCAAGT 840
Db 781 ATGCAAGAGCAGGTCATGAAGCACTTTATCGAGATTGACCGGGGAAAGTCTTGTCAAGT 840
Qy 841 TTTGTTAAAAAATGATCAAACTGCTCAGTCTAGCTATGTGGAGATCAAGCGAGTTTA 900
Db 841 TTTGTTAAAAAATGATCAAACTGCTCAGTCTAGCTATGTGGAGATCAAGCGAGTTTA 900
Qy 901 GTAGCACTTTTAGAAAAAATAG 921
Db 901 GTAGCACTTTTAGAAAAAATAG 921

RESULT 9
US-09-815-242-9482
; Sequence 9482, Application US/09815242
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-10-23
; PRIOR FILING DATE: 2000-11-27
; PRIOR FILING DATE: 2000-11-27
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9482
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(921)
US-09-815-242-9482

Query Match 99.0%; Score 911.4; DB 31; Length 921;
Best Local Similarity 99.3%; Pred. No. 2.2e-268;
Matches 915; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGACTAAACAGCCCTTTTATTTGCTGCTCAAGGTGCCAGTATCTAGGGATGGACGG 60
DB 1 ATGACTAAACAGCCCTTTTATTTGCTGCTCAAGGTGCCAGTATCTAGGGATGGACGG 60

QY 61 GATTCTATGATCAGTATCGGATTTCAAGAAACGATTGATCGAGCGAGTCAAGTGTCTC 120
DB 61 GATTCTATGATCAGTATCGGATTTCAAGAAACGATTGATCGAGCGAGTCAAGTGTCTC 120

QY 121 GGTATGATTTAGTATCTCATCGATACGGAAGAGACAACTCAATCAGACCCGCTAT 180
DB 121 GGTATGATTTAGTATCTCATCGATACGGAAGAGACAACTCAATCAGACCCGCTAT 180

QY 181 ACCCAACGACGCTTCTAGGACTTCGGTGTCTATCTACCGTTTATGCAAGAAAGGCG 240
DB 181 ACCCAACGACGCTTCTAGGACTTCGGTGTCTATCTACCGTTTATGCAAGAAAGGCG 240

QY 241 TATCAGCCTGATATGCTGCTGTTTCTCTTGGAGATATCTGCGCTTGGTGGCAAGC 300
DB 241 TATCAGCCTGATATGCTGCTGTTTCTCTTGGAGATATCTGCGCTTGGTGGCAAGC 300

QY 301 GCGCCTTGGATTTGAAGATCGGTTGCTTGGTAGCTTAAGCTGGAGCCTTATATGAA 360
DB 301 GCGCCTTGGATTTGAAGATCGGTTGCTTGGTAGCTTAAGCTGGAGCCTTATATGAA 360

QY 361 GAAGCGGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 361 GAAGCGGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

QY 421 ATTGAAGAGCCTTCTCAAGAAAGCTTCTGAAGTGGAGTGGTGTCTTCCAGCCTATTA 480
DB 421 ATTGAAGAGCCTTCTCAAGAAAGCTTCTGAAGTGGAGTGGTGTCTTCCAGCCTATTA 480

QY 481 ACACCTGCAAAATCGTATCTGCTGAGAGAGTGGTGTGAGTGTGATCGAGCGTGAAC 540
DB 481 ACACCTGCAAAATCGTATCTGCTGAGAGAGTGGTGTGAGTGTGATCGAGCGTGAAC 540

QY 541 TTGCAAGAGCAGGTGCCAAAGCTTGATTTCTTCTTAAAGTGTGAGTGTGCTTCAAC 600
DB 541 TTGCAAGAGCAGGTGCCAAAGCTTGATTTCTTCTTAAAGTGTGAGTGTGCTTCAAC 600

QY 601 GCTCTCCTTGAAGCTGCTAGCAGAACTAGCTGAAACTCTAGCTCAGTAAAGTGTTC 660
DB 601 GCTCTCCTTGAAGCTGCTAGCAGAACTAGCTGAAACTCTAGCTCAGTAAAGTGTTC 660

QY 661 GATTTTACTTGTCCCTAGTGTGCAATACAGAGCTGCTGCTGATGCAAGAGGACAT 720
DB 661 GATTTTACTTGTCCCTAGTGTGCAATACAGAGCTGCTGCTGATGCAAGAGGACAT 720

QY 721 GCTCAGCTCTTGAAGCTGCTAGGAAACCCGTTGCTTCTATGAAAGTATTTGGGTC 780
DB 721 GCTCAGCTCTTGAAGCTGCTAGGAAACCCGTTGCTTCTATGAAAGTATTTGGGTC 780

QY 781 ATGCAAGAGCAGGCTAGGAACTTATCGAGATGGACCGGGAAGTCTTGTGAGGT 840
DB 781 ATGCAAGAGCAGGCTAGGAACTTATCGAGATGGACCGGGAAGTCTTGTGAGGT 840

QY 841 TTGTTTAAAAAATGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGGTTTA 900
DB 841 TTGTTTAAAAAATGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGGTTTA 900

QY 901 GTAGCCTTTAGAAAAATAG 921
DB 901 GTAGCCTTTAGAAAAATAG 921

RESULT 10
US-10-072-851-9482
; Sequence 9482 Application US/10072851
; GENERAL INFORMATION:

APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
APPLICANT: Foulkes, J. Gordon
APPLICANT: Zamudio, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Orlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Yamamoto, John D.
APPLICANT: Roemer, Terry
APPLICANT: Jiang, Bo
APPLICANT: Boone, Charles
APPLICANT: Bussey, Howard
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028A
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9482
LENGTH: 921
TYPE: DNA
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(921)
US-10-072-851-9482

Query Match 99.0%; Score 911.4; DB 39; Length 921;
Best Local Similarity 99.3%; Pred. No. 2.2e-268;
Matches 915; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGACTAAACAGCCCTTTTATTTGCTGCTCAAGGTGCCAGTATCTAGGGATGGACGG 60
DB 1 ATGACTAAACAGCCCTTTTATTTGCTGCTCAAGGTGCCAGTATCTAGGGATGGACGG 60

QY 61 GATTCTATGATCAGTATCGGATTTCAAGAAACGATTGATCGAGCGAGTCAAGTGTCTC 120
DB 61 GATTCTATGATCAGTATCGGATTTCAAGAAACGATTGATCGAGCGAGTCAAGTGTCTC 120

QY 121 GGTATGATTTAGTATCTCATCGATACGGAAGAGACAACTCAATCAGACCCGCTAT 180
DB 121 GGTATGATTTAGTATCTCATCGATACGGAAGAGACAACTCAATCAGACCCGCTAT 180

QY 181 ACCCAACGACGCTTCTAGGACTTCGGTGTCTATCTGAGTGTGATCGAGCGTGAAC 240
DB 181 ACCCAACGACGCTTCTAGGACTTCGGTGTCTATCTGAGTGTGATCGAGCGTGAAC 240

QY 241 TATCAGCCTGATATGCTGCTGTTTCTCTTGGAGATATCTGCTTGGTGGCAAGC 300
DB 241 TATCAGCCTGATATGCTGCTGTTTCTCTTGGAGATATCTGCTTGGTGGCAAGC 300

QY 301 GCGCCTTGGATTTGAAGATCGGTTGCTTGGTAGCTTAAGCTGGAGCCTTATATGAA 360
DB 301 GCGCCTTGGATTTGAAGATCGGTTGCTTGGTAGCTTAAGCTGGAGCCTTATATGAA 360

QY 361 GAAGCGGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 361 GAAGCGGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

QY 421 ATTGAAGAGCCTTCTCAAGAAAGCTTCTGAAGTGGAGTGGTGTGAGTGTGATCGAG 480
DB 421 ATTGAAGAGCCTTCTCAAGAAAGCTTCTGAAGTGGAGTGGTGTGAGTGTGATCGAG 480

QY 481 ACACCTGCAAAATCGTATCTGCTGAGAGAGTGGTGTGAGTGTGATCGAGCGTGAAC 540
DB 481 ACACCTGCAAAATCGTATCTGCTGAGAGAGTGGTGTGAGTGTGATCGAGCGTGAAC 540

QY 541 TTGCAAGAGCAGGTGCCAAAGCTTGATTTCTTCTTAAAGTGTGAGTGTGCTTCAAC 600
DB 541 TTGCAAGAGCAGGTGCCAAAGCTTGATTTCTTCTTAAAGTGTGAGTGTGCTTCAAC 600

Db 541 TTGCAAGAGCAGGTGCCAAACGCTTGATTCCTCTTAAGGTGTCAGTCCCTTTCACCC 600
QY GCTCTCCTTGAGCCTGTAGCAGAACTAGCTGAAACTCTAGCTCAGGTAAGTTTTTCA 660
Db GCTCTCCTTGAACTGCTAGCAGAACTAGCTGAAACTCTAGCTCAGGTAAGTTTTCA 660
QY GATTTTACTTGTCCCTAGTCGGCAATACAGAACTGCTGTGATGCAAAAAGAGACATT 720
Db GATTTTACTTGTCCCTAGTCGGCAATACAGAACTGCTGTGATGCAAAAAGAGACATT 720
QY GCTCAGCTCTTGAGCCTGAGTCAAGGAAACCCGTTCTTCTATGAAAGTATTGGGGTC 780
Db GCTCAGCTCTTGAGCCTGAGTCAAGGAAACCCGTTCTTCTATGAAAGTATTGGGGTC 780
QY ATGCAAGAGCAGCATAGCAACTTTATCGAATTTGAGACCGGGGAAAGTCTTGTACGTT 840
Db ATGCAAGAGCAGCATAGCAACTTTATCGAATTTGAGACCGGGGAAAGTCTTGTACGTT 840
QY TTTGTTAAAAAATTGATCAAACTGCTCAGTTAGTCTCATGTGGAAGATCAAGCGAGTTA 900
Db TTTGTTAAAAAATTGATCAAACTGCTCAGTTAGTCTCATGTGGAAGATCAAGCGAGTTA 900
QY GTAGCACTTTTAGAAAAATAG 921
Db GTAGCACTTTTAGAAAAATAG 921

RESULT 11

PCT-US97-22578-43
Sequence 43, Application PC/TUS9722578
GENERAL INFORMATION:
APPLICANT: Baltz, Richard H.
APPLICANT: Burgett, Stanley G.
APPLICANT: DeHoff, Bradley S.
APPLICANT: Jaskunas Jr., Stanley R.
APPLICANT: Mills, Bradley J.
APPLICANT: Norris, Franklin H.
APPLICANT: Peery, Robert B.
APPLICANT: Rostek Jr., Paul R.
APPLICANT: Skatrud, Paul L.
APPLICANT: Smith, Michele C.
APPLICANT: Rocky, Pamela K.
APPLICANT: Young-Bellido, Michele
TITLE OF INVENTION: Streptococcus Pneumoniae DNA Sequences
NUMBER OF SEQUENCES: 228
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: U.S.
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/22578
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-11162
TELEPHONE: 317-276-3334
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 3580 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US97-22578-43
Query Match 99.0%; Score 911.4; DB 1; Length 3580;
Best Local Similarity 99.3%; Pred. No. 4.1e-268;
Matches 915; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ATGACTAAACAGACGCTTTTATTTCCTGCTCAAGGTGCCAGTATCTAGGATGGGACGG 60
Db 718 ATGACTAAACAGACGCTTTTATTTCCTGCTCAAGGTGCCAGTATCTAGGATGGGACGG 777
QY 61 GATTTCTATGATCAGTATCCGATTTCAAGAAAGATGATCGAGCGAGTCAGTGCTC 120
Db 778 GATTTCTATGATCAGTATCCGATTTTAAAGAAACGATTGATCGAGCGAGTCAGTGCTA 837
QY 121 GGTATGATTTACGTTATCTCATCGATACGGAAGAGCAAACTCAATCAGACCCGCTAT 180
Db 838 GGTATGATTTACGTTATCTCATCGATACGGAAGAGCAAACTCAATCAGACCCGCTAT 897
QY 181 AGCAACCAAGCAATCTTAGCGACTTTCGGTTGCTATCTACCGTTTATTCAGAAAAAGGC 240
Db 898 AGCAACCAAGCAATCTTAGCGACTTTCGGTTGCTATCTACCGTTTATTCAGAAAAAGGC 957
QY 241 TATCAGCCCTGATATGTTGCTGTTTCTCTTGGAGATATCTCTGCTTGGTGCACAGC 300
Db 958 TATCAGCCCTGATATGTTGCTGTTTCTCTTGGAGATATCTCTGCTTGGTGCACAGC 1017
QY 301 GCGCCCTTGGATTTTGAAGATGCGGTTGCTTGGTAGTAAAGCGTGAGACCTTATATGAA 360
Db 1018 GCGCCCTTGGATTTTGAAGATGCGGTTGCTTGGTAGTAAAGCGTGAGACCTTATATGAA 1077
QY 361 GAAGCGGCTCTGCTGACTCTGGCAAGATGTTAGCAGTCTCAATACGCCAGTAGAGTC 420
Db 1078 GAAGCGGCTCTGCTGACTCTGGCAAGATGTTAGCAGTCTCAATACGCCAGTAGAGTC 1137
QY 421 ATTGAAGAAGCGCTGCAAAAAGCTTCTGAACTGGAGTGGTTACTCCAGCCCAACTATAAC 480
Db 1138 ATTGAAGAAGCGCTGCAAAAAGCTTCTGAACTGGAGTGGTTACTCCAGCCCAACTATAAC 1197
QY 481 ACACCTGCACAAATCGTCAATCTGCGAAGTGGTTGAGTTCAGTTCAGACGGTTGAACTT 540
Db 1198 ACACCTGCACAAATCGTCAATCTGCGAAGTGGTTGAGTTCAGTTCAGACGGTTGAACTT 1257
QY 541 TTGCAAGAAGCAGGTGCCAAACGCTTTCCTCTTAAAGGTGTCAGGTCCTTTTCACACC 600
Db 1258 TTGCAAGAAGCAGGTGCCAAACGCTTTCCTCTTAAAGGTGTCAGGTCCTTTTCACACC 1317
QY 601 GCTCTCCTTGAGCCTGTAGCCAGAACTAGCTGAAACTCTAGCTCAGGTAAGTTTTTCA 660
Db 1318 GCTCTCCTTGAGCCTGTAGCCAGAACTAGCTGAAACTCTAGCTCAGGTAAGTTTTTCA 1377
QY 661 GATTTTACTTGTCCCTAGTCGGCAATACAGAACTGCTGTGATGCAAAAAGAGACATT 720
Db 1378 GATTTTACTTGTCCCTAGTCGGCAATACAGAACTGCTGTGATGCAAAAAGAGACATT 1437
QY 721 GCTCAGCTCTTGAGCCTGAGTCAAGGAAACCCGTTCTTCTATGAAAGTATTGGGGTC 780
Db 1438 GCTCAGCTCTTGAGCCTGAGTCAAGGAAACCCGTTCTTCTATGAAAGTATTGGGGTC 1497
QY 781 ATGCAAGAAGCAGCATAGCAACTTTATCGAATTTGAGACCGGGGAAAGTCTTGTACGTT 840
Db 1498 ATGCAAGAAGCAGCATAGCAACTTTATCGAATTTGAGACCGGGGAAAGTCTTGTACGTT 1557
QY 841 TTTGTTAAAAAATTGATCAAACTGCTCAGTTAGTCTCATGTGGAAGATCAAGCGAGTTA 900
Db 1558 TTTGTTAAAAAATTGATCAAACTGCTCAGTTAGTCTCATGTGGAAGATCAAGCGAGTTA 1617
QY 901 GTAGCACTTTTAGAAAAATAG 921
Db 1618 GTAGCACTTTTAGAAAAATAG 1638

RESULT 12
US-60-068-175-555
; Sequence 555, Application US/60068175
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert E.
; APPLICANT: Corley, Neil C.
; APPLICANT: Russo, Frank D.
; APPLICANT: Hann, Amy L.
; APPLICANT: Heath, Joe D.
; APPLICANT: Finney, Gregory L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF STREPTOCOCCUS PNEUMONIAE
; TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
; NUMBER OF SEQUENCES: 1175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/068,175
; FILING DATE: HEREWITH
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PM-0009-2 P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-416
; INFORMATION FOR SEQ ID NO: 555:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9753 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: genomic DNA
; IMMEDIATE SOURCE:
; CLONE: SPN2C557
US-60-068-175-555
Query Match 99.0%; Score 911.4; DB 50; Length 9753;
Best Local Similarity 99.3%; Pred. No. 6.5e-268;
Matches 915; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ATGACTAAACAGCCCTTTTATTGCTGTCAGGTGCCAGTATCTAGGATGGACGG 60
Db 1234 ATGACTAAACAGCCCTTTTATTGCTGTCAGGTGCCAGTATCTAGGATGGACGG 1293
QY 61 GATTTCATGATCAGTATCCGATTGTCAGGAAGAAAGATTGATCGAGCAGTCAAGTGCTC 120
Db 1294 GATTTCATGATCAGTATCCGATTGTCAGGAAGAAAGATTGATCGAGCAGTCAAGTGCTC 1353
QY 121 GGTATGATTAGCTTATCTCATGATCGGAAGAAAGAACTCAATCAGACCCGCTAT 180
Db 1354 GGTATGATTAGCTTATCTCATGATCGGAAGAAAGAACTCAATCAGACCCGCTAT 1413
QY 181 AGCAACACGACATTCAGGATTCGCTGTTGCTATCTACCGTTTATTGCAAGAAAGGCG 240
Db 1414 ACACAACACGACATTCAGGATTCGCTGTTGCTATCTACCGTTTATTGCAAGAAAGGCG 1473
QY 241 TATCAGCCGATGATGCTGCTGTTGCTCTTGGAGATATCTCTGCCCTTGTGGCAAGC 300
Db 1474 TATCAGCCGATGATGCTGCTGTTGCTCTTGGAGATATCTCTGCCCTTGTGGCAAGC 1533

QY 301 GGCGCCTTGATTTTGAAGATGCGGTTGCTTGGTAGCTAAGCGTGAGACCTATATGGAA 360
Db 1534 GGCGCCTTGATTTTGAAGATGCGGTTGCTTGGTAGCTAAGCGTGAGACCTATATGGAA 1593
QY 361 GAAGCGGCTCCTGCTGACTCTGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTC 420
Db 1594 GAAGCGGCTCCTGCTGACTCTGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTC 1653
QY 421 ATTGAAGAAGCCTGTCAAAAGCTTCTGAACCTTGGAGTGGTACTCCAGCAACTATAAC 480
Db 1654 ATTGAAGAAGCCTGTCAAAAGCTTCTGAACCTTGGAGTGGTACTCCAGCAACTATAAC 1713
QY 481 ACACCTGCAAAATGTCATTGCTGGAGAAGTGGTTGCAAGTTCATCGAGCGGTGAACTT 540
Db 1714 ACACCTGCAAAATGTCATTGCTGGAGAAGTGGTTGCAAGTTCATCGAGCGGTGAACTT 1773
QY 541 TTGCAAGAAGCAGGTGCCAAACGCTTCTTTAAGGTGTCAGGTCCCTTTTCACACC 600
Db 1774 TTGCAAGAAGCAGGTGCCAAACGCTTCTTTAAGGTGTCAGGTCCCTTTTCACACC 1833
QY 601 GCTCTCTTGAGCCTGCTAGCCAGAACTAGCTGAACTCTAGCTCAGGTAACTTTTCA 660
Db 1834 GCTCTCTTGAGCCTGCTAGCCAGAACTAGCTGAACTCTAGCTCAGGTAACTTTTCA 1893
QY 661 GATTTTACTTGTCCCTAGTTCGCAATACAGAACTCTGTCATGATGCAAAAGAGGACAT 720
Db 1894 GATTTTACTTGTCCCTAGTTCGCAATACAGAACTCTGTCATGATGCAAAAGAGGACAT 1953
QY 721 GCTCAGCTCTTGAGCGGTGCTAGGTCAGGAACCGCTTCTTATGAAAGTATTTGGGTC 780
Db 1954 GCTCAGCTCTTGAGCGGTGCTAGGTCAGGAACCGCTTCTTATGAAAGTATTTGGGTC 2013
QY 781 ATGCAAGAAGCAGGCATTAAGCAACTTATCGAGATTGGACCGGGGAAAGTCTTGTGAGGT 840
Db 2014 ATGCAAGAAGCAGGCATTAAGCAACTTATCGAGATTGGACCGGGGAAAGTCTTGTGAGGT 2073
QY 841 TTTGTTAAAAAAATTGATCAAACTGCTCACTAGCTCATGTCATGTCGAAAGTCAAGCGAGTTTA 900
Db 2074 TTTGTTAAAAAAATTGATCAAACTGCTCACTAGCTCATGTCATGTCGAAAGTCAAGCGAGTTTA 2133
QY 901 GTAGCACTTTTAAAAAATAG 921
Db 2134 GTAGCACTTTTAAAAAATAG 2154

RESULT 13
US-09-752-069A-256
; Sequence 256, Application US/09752069A
; GENERAL INFORMATION:
; APPLICANT: Dougherty, Thomas J.
; APPLICANT: Pucci, Michael J.
; APPLICANT: Dougherty, Brian A.
; APPLICANT: Davison, Daniel B.
; APPLICANT: Brucoleri, Robert E.
; APPLICANT: Thanassi, Jane A.
; APPLICANT: Farmer II, Bennett T.
; TITLE OF INVENTION: NOVEL BACTERIAL GENES AND PROTEINS THAT ARE ESSENTIAL
; TITLE OF INVENTION: FOR CELL VIABILITY AND THEIR USES
; FILE REFERENCE: D0001NP
; CURRENT APPLICATION NUMBER: US/09/752,069A
; PRIOR FILING DATE: 2000-12-29
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 256
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-752-069A-256

Query Match 98.8%; Score 908.4; DB 29; Length 945;
Best Local Similarity 99.3%; Pred. No. 1.8e-267;

Matches 912; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGACTAAACAGCCCTTTTATTTGCTGCTCAAGTGCCAGTATCTAGGATGGGACGG 60

Db 1 ATGACTAAACAGCCCTTTTATTTGCTGCTCAAGTGCCAGTATCTAGGATGGGACGG 60

QY 61 GATTCTTATGATCAGTATCCGATTTCAAGAAAGCATGATCGAGCGAGTCAGGTGCTC 120

Db 61 GATTCTTATGATCAGTATCCGATTTCAAGAAAGCATGATCGAGCGAGTCAGGTGCTC 120

QY 121 GGTATGATTTATGATTTATCTATCATACGAGGAGAGCAAACTCAATCAGACCGCTAT 180

Db 121 GGTATGATTTATGATTTATCTATCATACGAGGAGAGCAAACTCAATCAGACCGCTAT 180

QY 181 ACGCAACAGCCATTTAGAGCTTCGGTTGCTATCTACCGTTTATTCGAAGAAAGGCG 240

Db 181 ACGCAACAGCCATTTAGAGCTTCGGTTGCTATCTACCGTTTATTCGAAGAAAGGCG 240

QY 241 TATCAGCTGATATGGTTCCTGCTGCTTCTCTGAGATATCTCTGCTTGGTGGCAGC 300

Db 241 TATCAGCTGATATGGTTCCTGCTGCTTCTCTGAGATATCTCTGCTTGGTGGCAGC 300

QY 301 GCGGCTTGGATTTTGAAGATCGGTTGCTTGGTAGCTAAGCGTGGAGCCATATGAA 360

Db 301 GCGGCTTGGATTTTGAAGATCGGTTGCTTGGTAGCTAAGCGTGGAGCCATATGAA 360

QY 361 GAAGCGGCTCTGCTGATCTGCGAAGATGGTAGCAGTTCTCAATACCCAGTAGAGTC 420

Db 361 GAAGCGGCTCTGCTGATCTGCGAAGATGGTAGCAGTTCTCAATACCCAGTAGAGTC 420

QY 421 ATTGAAGAGCTGTCAAAAGCTTCTGAACCTTGGAGTGGTACTCCAGGCAACTATAAC 480

Db 421 ATTGAAGAGCTGTCAAAAGCTTCTGAACCTTGGAGTGGTACTCCAGGCAACTATAAC 480

QY 481 ACACCTGACAAATCGTCAATCTCTCGAAGAGTGGTTGCAAGTATCGAGCGGTTGAACTT 540

Db 481 ACACCTGACAAATCGTCAATCTCTCGAAGAGTGGTTGCAAGTATCGAGCGGTTGAACTT 540

QY 541 TTGCAAGAGCAGGTGCCAAGCGTTGATCTCTTAAGGTGTCAGGTCCCTTTTCACAC 600

Db 541 TTGCAAGAGCAGGTGCCAAGCGTTGATCTCTTAAGGTGTCAGGTCCCTTTTCACAC 600

QY 601 GCTCTCTTGAACCTGCTAGCCAGAGAACTAGCTGAAACTCTAGCTCAGGTAAGTTTCA 660

Db 601 GCTCTCTTGAACCTGCTAGCCAGAGAACTAGCTGAAACTCTAGCTCAGGTAAGTTTCA 660

QY 661 GATTCTTACTTGTCCCTAGTGGGCAATACAGAGCTGCTGATGCAAGAAAGAGACATT 720

Db 661 GATTCTTACTTGTCCCTAGTGGGCAATACAGAGCTGCTGATGCAAGAAAGAGACATT 720

QY 721 GCTCAGCTCTTCAACCGTCAGGTCAAGAACCCGTTTCTATGAAAGTATTTGGGTC 780

Db 721 GCTCAGCTCTTCAACCGTCAGGTCAAGAACCCGTTTCTATGAAAGTATTTGGGTC 780

QY 781 ATGCAAGAGCAGGATAGCAACTTTATCGAGATGACCGGGGAAAGTTTGTACAGGT 840

Db 781 ATGCAAGAGCAGGATAGCAACTTTATCGAGATGACCGGGGAAAGTTTGTACAGGT 840

QY 841 TTTGTTTAAATTAATGATCAACTCTCCTACCTAGCTCATGTGGAAGTCAGGAGTTTA 900

Db 841 TTTGTTTAAATTAATGATCAACTCTCCTACCTAGCTCATGTGGAAGTCAGGAGTTTA 900

QY 901 GTAGCCTTTTAAAAA 918

Db 901 GTAGCCTTTTAAAAA 918

RESULT 14

US-60-061-998-494

; Sequence 494, Application US/60061998

; GENERAL INFORMATION:

; APPLICANT: LAGACE, ROBERT E.

; APPLICANT: CORLEY, NEIL C.

APPLICANT: RUSSO, FRANK D.
 APPLICANT: HANN, AMY L.
 APPLICANT: HEATH, JOE D.
 APPLICANT: FINNEY, GREGORY L.
 TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF STREPTOCOCCUS PNEUMONIAE
 TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
 NUMBER OF SEQUENCES: 797
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/60/061,998
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: CERRONE, MICHAEL C.
 REGISTRATION NUMBER: 39,132
 REFERENCE/DOCKET NUMBER: PM-0006-2P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 494:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5963 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 IMMEDIATE SOURCE:
 CLONE: SPN1c499
 US-60-061-998-494

Query Match 96.8%; Score 891.6; DB 50; Length 5963;
 Best Local Similarity 98.9%; Pred. No. 6.2e-262;
 Matches 908; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 1 ATGACTAAACAGCCCTTTTATTTGCTGCTCAAGTGCCAGTATCTAGGATGGGACGG 60

Db 2919 ATGACTAAACAGCCCTTTTATTTGCTGCTCAAGTGCCAGTATCTAGGATGGGACGG 2978

QY 61 GATTTCTATGATCAGTATCCGATTTGTCAAAGAAACGATTGATCGAGCGAGTCAGGTGCTC 120

Db 2979 GATTTCTATGATCAGTATCCGATTTGTCAAAGAAACGATTGATCGAGCGAGTCAGGTGCTC 3038

QY 121 GGTATGATTTAGCTTATCTCATCGATACGGAAGAAAGCAAACTCAATCAGACCCGCTAT 180

Db 3039 GGTATGATTTAGCTTATCTCATCGATACGGAAGAAAGCAAACTCAATCAGACCCGCTAT 3098

QY 181 ACCCAACAGCCATTTAGCGACTTCGGTTGCTATCTACCGTTTATTCGAAGAAAGGCG 240

Db 3099 ACCCAACAGCCATTTAGCGACTTCGGTTGCTATCTACCGTTTATTCGAAGAAAGGCG 3158

QY 241 TATCAGCCTGATATGGTTGCTGCTTCTCTTGGAGAAATCTCTGCTTGGTGGCAAGC 300

Db 3159 TATCAGCCTGATATGGTTGCTGCTTCTCTTGGAGAAATCTCTGCTTGGTGGCAAGC 3218

QY 301 GCGGCTTGGATTTTGAAGATCGGTTGCTTGGTAGCTAAGCGTGGAGCCCTATATGAA 360

Db 3219 GCGGCTTGGATTTTGAAGATCGGTTGCTTGGTAGCTAAGCGTGGAGCCCTATATGAA 3278

QY 361 GAAGCGGCTCCTGCTGACTCTGCAAGATGGTAGCAGTTTCTCAATACGCCAGCTAGAGGTC 420

Db 3279 GAAGCGGCTCCTGCTGACTCTGCAAGATGGTAGCAGTTTCTCAATACGCCAGCTAGAGGTC 3338


```
QY 421 ATTGAAGAAGCTGCTCAAAAGCTTCTGAACCTTGGAGTGGTTACTCCAGCCCACTATAAC 480
|
|
|
Db 3339 ATTGAAGAAGCTGCTCAAAAGCTTCTGAACCTTGGAGTGGTTACTCCAGCCCACTATAAC 3398
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|
|
QY 481 ACACCT-GCAAAATGCTATTGCTGGAGAAGTGGTTGCAAGTTGATCGAGCGGTTGAACT 539
|
|
|
Db 3399 ACACCTGGCAAAATGCTATTGCTGGAGAAGTGGTTGCAAGTTGATCGAGCGGTTGAACT 3458
|
|
|
QY 540 TTTCGAAGAAGCAGTCCCAAGCTTGAATTCCTCTTAAGGTGTCAGGTCCCTTTCCACAC 599
|
|
|
Db 3459 TTTCGAAGAAGCAGTCCCAAGCTTGAATTCCTCTTAAGGTGTCAGGTCCCTTTCCACAC 3518
|
|
|
QY 600 CGCTCTCCTTTAGCCTCTAGCCAGAAACTAGCTGAAACTCTAGCTCAGSTAACTTTTTC 659
|
|
|
Db 3519 CTCTCTCCTTTGAACCTCTAGCCAGAAACTAGCTGAAACTCTGGCTCAGSTAACTTTTTC 3578
|
|
|
QY 660 AGATTTTACTTGCCCTAGTCGGCAATACAGAGCTGCTGATGCMAAAGAGGACAT 719
|
|
|
Db 3579 AGATTTTACTTGCCCTAGTCGGCAATACAGAGCTGCTGATGCMAAAGAGGACAT 3638
|
|
|
QY 720 TGCTCAGCTCTTGACGGCTCAGSTCAAGGAACCGTTCTGTTCTATGAAAGTATTGGGGT 779
|
|
|
Db 3639 TGCTCAGCTCTTGACGGCTCAGSTCAAGGAACCGTTCTGTTCTATGAAAGTATTGGGGT 3698
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|
|
QY 780 CATGCAAGAAGCAGGCATAAGCACTTTATCGAGATTGGACCGGGGAAAGTCTTTGTCAGG 839
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|
|
Db 3699 CATGCAAGAAGCAGGCATAAGCACTTTATCGAGATTGGACCGGGGAAAGTCTTTGTCAGG 3758
|
|
|
QY 840 TTTTGTATAAAATTTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTT 899
|
|
|
Db 3759 TTTTGTATAAAATTTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTT 3818
|
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|
QY 900 AGTAGCACTTTTAGAAAA 917
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|
Db 3819 AGTAGCACTTTTAGAAAAA 3836
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|
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RESULT 15

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US-09-308-397-5
; Sequence 5, Application US/09308397
; GENERAL INFORMATION:
; APPLICANT: Gentry, Daniel R.
; APPLICANT: Lonsdale, John T.
; APPLICANT: Payne, David J.
; APPLICANT: Pearson, Stewart C.
; APPLICANT: Van Aller, Glenn
; TITLE OF INVENTION: Novel FabD
; FILE REFERENCE: P50593
; CURRENT APPLICATION NUMBER: US/09/308,397
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: US 60/031,160
; EARLIER FILING DATE: 1996-11-18
; EARLIER APPLICATION NUMBER: PCT/US97/20992
; EARLIER FILING DATE: 1997-11-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-308-397-5
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Query Match 57.5%; Score 529.4; DB 17; Length 547;
Best Local Similarity 98.0%; Pred. No. 3.8e-151;
Matches 536; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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QY 372 TGCTGACTCTGGCAAGATGGTAGAGTTCTCAATACGCCAGTAGAGTCAATTGAAAGC 431
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Db 1 TGCTGAATTTGGCAAGATGGTAGAGTTCTCAATACGCCAGTAGAGTCAATTGAAAGC 60
|
|
|
QY 432 CTGTCAAAAGCTTCTGAACCTTGGAGTGGTTACTCCAGCCCACTATAACACACTGCACA 491
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|
|
Db 61 CTGTCAAAAGCTTCTGAACCTTGGAGTGGTTACTCCAGCCCACTATAACACACTGCACA 120
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QY 492 AATCGTCATTCTCGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACCTTTGCAAGAAGC 551
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|
|
Db 121 AATCGTCATTCTCGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACCTTTGCAAGAAGC 180
|
|
|
QY 552 AGGTGCCAAACGCTTGATTCTCTTAAGGTGTCAGGTCCCTTTCCACCCGCTCTCCTTTGA 611
|
|
|
Db 181 AGGTGCCAAACGCTTGATTCTCTTAAGGTGTCAGGTCCCTTTCCACCCGCTCTCCTTTGA 240
|
|
|
QY 612 GCCTGCTAGCCAGAAACTAGCTGAAACTCTAGCTCAGSTAAGTTTTCAGATTCTACTTG 671
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|
|
Db 241 GCCTGCTAGCCAGAAACTAGCTGAAACTCTAGCTCAGSTAAGTTTTCAGATTCTACTTG 300
|
|
|
QY 672 TCCCTTAGTCCGGCAATACAGAAGCTGCTGATGCAAAAAGAGGACATTTGCTCAGCTCTT 731
|
|
|
Db 301 TCCCTTAGTCCGGCAATACAGAAGCTGCTGATGCAAAAAGAGGACATTTGCTCAGCTCTT 360
|
|
|
QY 732 GACGGTTCAGTCAAGNAACCCGTTCTGTTCTATGAAAGTATTGGGGTCATGCAAGAAGC 791
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|
|
Db 361 GACGGTTCAGTCAAGNAACCCGTTCTGTTCTATGAAAGTATTGGGGTCATGCAAGAAGC 420
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|
|
QY 792 AGGCATAAGCAACTTTATCGAGATTGGACCGGGGAAAAGTCTTTGTCAGGTTTGTAAAAA 851
|
|
|
Db 421 AGGCATAAGCAACTTTATCGAGATTGGACCGGGGAAAAGTCTTTGTCAGGTTTGTAAAAA 480
|
|
|
QY 852 AATTGATCAAACTGCTCAGCTTATGCTGATGCAAAAAGATCAAGCGAGTTTAGTAGACTTTT 911
|
|
|
Db 481 AATTGATCAAACTGCTCAGCTTATGCTGATGCAAAAAGATCAAGCGAGTTTAGTAGACTTTT 540
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|
QY 912 AGAAAAA 918
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Db 541 AGAAAAA 547
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|
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Search completed: June 11, 2003, 19:45:30
Job time : 2192 secs


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; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; US-10-282-122A-37621

Query Match          99.0%; Score 911.4; DB 9; Length 921;
Best Local Similarity 99.3%; Pred. No. 66-270;
Matches 915; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGACTAAACAGCCCTTTTATTTGCTGCTCAAGGTGCCAGTATCTAGGATGGACGG 60
DB 1 ATGACTAAACAGCCCTTTTATTTGCTGCTCAAGGTGCCAGTATCTAGGATGGACGG 60
QY 61 GATTTCTATGATCAGTATCCGATTTGTCAGGAAAGACGATGATCGAGCGAGTCAGGTGCTC 120
DB 61 GATTTCTATGATCAGTATCCGATTTGTCAGGAAAGACGATGATCGAGCGAGTCAGGTGCTA 120
QY 121 GGTATGATTTACGTTATCTCATCGATACGGAAGACAACTCAATCAGACCGCGTAT 180
DB 121 GGTATGATTTACGTTATCTCATCGATACGGAAGACAACTCAATCAGACCGCGTAT 180
QY 181 ACACAACAGCCATCTACGACTTCGGTGTCTATCTACCGTTTATTGCAAGAAAGGCG 240
DB 181 ACACAACAGCCATCTACGACTTCGGTGTCTATCTACCGTTTATTGCAAGAAAGGCG 240
QY 241 TATCAGCCTGATATGGTTCCTGTTGCTCTTGAGAAATCTCTGCTTGGTGGCAAGC 300
DB 241 TATCAGCCTGATATGGTTCCTGTTGCTCTTGAGAAATCTCTGCTTGGTGGCAAGC 300
QY 301 GCGCCCTCGATTTTGAAGATCGGTTGCTTGGTAGCTACGCGTGGAGCCATATGGAA 360
DB 301 GCGCCCTCGATTTTGAAGATCGGTTGCTTGGTAGCTACGCGTGGAGCCATATGGAA 360
QY 361 GAAGCGGCTCCTGCTGACTCTGCAAGATGTTAGAGTCTCAATACCCAGTAGAGTGC 420
DB 361 GAAGCGGCTCCTGCTGACTCTGCAAGATGTTAGAGTCTCAATACCCAGTAGAGTGC 420
QY 421 ATTGAAGAGCCGTCTCAAAAGCTTCTGAACCTTGAGTGGTGTACTCCAGCCAACTATAAC 480
DB 421 ATTGAAGAGCCGTCTCAAAAGCTTCTGAACCTTGAGTGGTGTACTCCAGCCAACTATAAC 480
QY 481 ACACCTGCACAAATCGTCAATCTGCGAAGTGGTTCAGATGATCGAGCGGTTGAACCT 540
DB 481 ACACCTGCACAAATCGTCAATCTGCGAAGTGGTTCAGATGATCGAGCGGTTGAACCT 540
QY 541 TTGCAAGAGCAGGTGCCAAAGCTTGATCTCTTAAGGTGTCAGTCCCTTTCACACC 600
DB 541 TTGCAAGAGCAGGTGCCAAAGCTTGATCTCTTAAGGTGTCAGTCCCTTTCACACC 600
QY 601 GCTCTCTTGGAGCTCTAGCAGAACTAGCTGAACTCTAGCTCAGGTAACTTTTCA 660
DB 601 TCTCTCTTGGAGCTCTAGCAGAACTAGCTGAACTCTAGCTCAGGTAACTTTTCA 660
QY 661 GATTTTACTTGTCCCTAGTCGGCAATACAGAAGCTGTGTATGCCAAAAGAGACATTT 720
DB 661 GATTTTACTTGTCCCTAGTCGGCAATACAGAAGCTGTGTATGCCAAAAGAGACATTT 720
QY 721 GCTCAGCTCTGACGGTTCAGGTCAAGGAAACCGTTTCTATGAAGTATTGGGGTC 780
DB 721 GCTCAGCTCTGACGGTTCAGGTCAAGGAAACCGTTTCTATGAAGTATTGGGGTC 780
QY 781 ATCAAGAGCAGGCATACGAACTTTATCGAGATGGAACCGGGGAAAGTCTTGTGAGGT 840
DB 781 ATCAAGAGCAGGCATACGAACTTTATCGAGATGGAACCGGGGAAAGTCTTGTGAGGT 840
QY 841 TTTGTTTAAAAAATTTCATCAAACTGCTCATTAGCTCATGTGGAAGATCAAGCGAGTTTA 900
DB 841 TTTGTTTAAAAAATTTCATCAAACTGCTCATTAGCTCATGTGGAAGATCAAGCGAGTTTA 900
QY 901 GTAGCACTTTTAAAAAATAG 921
DB 901 GTAGCACTTTTAAAAAATAG 921

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QY 301 GGCGCCTTGGATTTGAAGATCGGGTTCCTTGGTAGCTAAGCGTGGAGCCTATATGGAA 360
 Db 301 GGTGCCATTTTCATTTGAAGATGSCCTAGCCTTGGTTCGAACAGCGTGGATTAAGAA 360
 QY 361 GAAGCGCTCTGCTGACTCTCGCAAGATGGTAGAGTTCTCAATACGCGAGTAGAGTC 420
 Db 361 ACAGCAGCACCGCTGGAGTGGGAAATGGTGTCTGTATGAATACTGACCCCTAGGCTC 420
 QY 421 ATTGAAGAGCCTGTCAAAAGCTTCTGAACCTTGGAGTGGTGTACTCCAGCCCACTATAAC 480
 Db 421 ATTGAAGAGCTTGTGAGAAAGCCAGCTCTAAAGCATTTGTAGTCCAGCTAATTAAT 480
 QY 481 ACACCTGCAAAATCGTATTCTCTGGAGAGTGGTGTGAGTTGATCGAGCGGTGAACCTT 540
 Db 481 ACTCCTTACACAAATCTTATGGTGGTGAAGTAGCAGCTGTGATTATGCTGTGGAACCTT 540
 QY 541 TTGCAAGAGCGGTCGCAAGCGCTTGATCTCTTTRAGGTGTCAGGTCCCTTTCACAC 600
 Db 541 TTAAGGGAGCTGGTAGTAAGCTTTGATTTCTCTTAAAGTTCTGGTCCCTTTCATACG 600
 QY 601 GCTCTCTTGGAGCTCTAGCAGAACTAGCTGAAACTCTAGCTCAGGTAACTTTTCA 660
 Db 601 GCTCTTTGAATCTGCTAGTCAAAATTTGGCTCAAGCTTTGGAATAATTAATTTCA 660
 QY 661 GATTTTACTTGTCCCTAGTCTGCAATACAGAGCTGCTGTGATCGAAGAGGACATTT 720
 Db 661 GATTTTCACTTCCACTAGTGGGACACTAAAGCTGAAATTTATGAAGGACAGGAGATT 720
 QY 721 GCTCAGCTCTGACGGCTCAGGTCAAGGAACCGCTTGGTTTCTATGAAGATTGGGGTC 780
 Db 721 AAACCTTTGCTGCTCAAGTCAAGAACCTTGTTCGCTTCTATGAATCTATTGCTGTA 780
 QY 781 ATGCAAGAGCGGCAATAGCAACTTTATCGAGATGGACCGGGAAGTCTTGTGAGGT 840
 Db 781 ATGCAAAATTTGGTGTGAATAAATATGTCGAAATTTGGACCTGGTAAAGTCTTGTAGTGT 840
 QY 841 TTGTGTAAGAAATTCATCAAACTGCTCACTAGCTCATGTGGAAGATCAAGCGAGTTA 900
 Db 841 TTGTGTAAGAAATTTGATTAATCTGCAAGATCTCAGCTGTGTAAGACTTAGTGTG 900
 QY 901 GTAGCACTTTTGAATA 917
 Db 901 CAGGCTTTCTAGATA 917

RESULT 3

US-10-282-122A-38525
 ; Sequence 38525, Application US/10282:122A
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Karl
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA.034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 38525
 ; LENGTH: 939
 ; TYPE: DNA
 ; ORGANISM: Streptococcus pyogenes
 US-10-282-122A-38525
 Query Match 47.7%; Score 439.4; DB 9; Length 939;
 Best Local Similarity 67.3%; Pred. No. 1.9e-124;
 Matches 620; Conservative 0; Mismatches 301; Indels 0; Gaps 0;
 QY 1 ATGACTAAACAGCCCTTTTATTTGCTGGTCAAGGTGCCAGATATCTAGGATGGACGG 60
 Db 1 ATGACAAAGACAGCCCTTTTATTTGCGGTCAAGGTGCTCAAAATTTAGGGATGGCAAG 60
 QY 61 GATTTCTATCATCAGATATCGATTGTCAAAGAACGATTGATCGAGGAGCTCAGGTGCTC 120
 Db 61 GATTTTATGATTAACCTTTGCTATTGTAAGAAAAACCTTTGATCAAGTAGTCAAGTATTG 120
 QY 121 GGTATGATTTAGCTTATCTCATCGATACGGAAGAAAGACAACTCAATCAGACCCGCTAT 180
 Db 121 GGTATGATTTAGCTTATCTCATCGATACGGAAGAAAGACAACTCAATCAGACCTAT 180
 QY 181 ACCCAACAGCCATCTTACGACTTCGGTGTGCTATCTACCGTTTATTCGAAAGAAAGGCG 240
 Db 181 ACCCAACAGCCATCTTACGACTTCGGTGTGCTATCTACCGTTTATTCGAAAGAAAGGCG 240
 QY 241 TATCAGCCTGATATGTTGCTGGTGTGCTCTCTCTTTGGAGAACTACTCTGCTTTGGTGGCAGC 300
 Db 241 GTTAAACCGGATATGGTAGCTGGTCTTCTCTTAGGAGAACTACTCAGCTTTGGTAGCATCA 300
 QY 301 GGCGCCTTGGATTTGAAGATCGGGTTCCTTGGTAGCTAAGCGTGGAGCCTATATGGAA 360
 Db 301 GGCGCCTTCTCTTTTGAAGATACCCCTATCCCTTAGTAGTAAAGAGAGCCGCTTGGAGGAG 360
 QY 361 GAAGCGGCTCTCTGCTGACTCTGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTC 420
 Db 361 GAAGCAGCACCAAGGATCTGGAAGATGGTTGCCGTTATGAATACAGACGTCGAAGTC 420
 QY 421 ATTGAAGAGCCTGTCAAAAGCTTCTGAACCTTGGAGTGGTGTACTCCAGCCCACTATAAC 480
 Db 421 ATCGAAGAGCTGTCAAAATAGCTGTGAACCATGGAGTGGTGTCTCCAGCAAACTATAAT 480
 QY 481 ACACCTGCAAAATCGTTCATTGCTGGAGAAAGTGGTTCAGTTGATCGAGCGGTGAACCTT 540
 Db 481 ACTCCTAGTCAAAATTTGATTTGGTGTGACAGATGCTGTGAACGTCGAGTGAACCTT 540
 QY 541 TTGCAAGAGCAGGTGCCAAACGCTTGATTTCTCTTTAAGGTGTCAAGTCCCTTTCACACC 600
 Db 541 TTAAGGAAAGAGGAGTTAAGCGCTTTAAATCCCTTTTAAACGCTGTCAAGTCCCTTTCACACT 600
 QY 601 GCTCTCCTTGGAGCTCTAGCAGAACTAGCTGAAACTCTAGCTCAGGTAACTTTTCA 660
 Db 601 GCTTTGTGTAACACAGCTAGCCCTTGTGGCTTAAAGATTGGAAGATTGGAAGATACAACTTCAGT 660
 QY 661 GATTTTACTTGTCCCTAGTCTGCAATACAGAGCTGCTGTGATCGAAGAGGACATTT 720
 Db 661 GACTTCAAGATTCCTTTGGTGTGTAATACCGAAGCTAAATATTATGAAAGAAAGACCGCTATC 720

QY 721 GCTCAGCTCTTGACGCGTCAAGGAACCGTTCGTTCTATGAAAGTATTGGGTC 780
Db 721 CCAGAACTATTAGCCGCTGAGTCATGAGCCCTGTTCTTTTATGACAGTGTGGACT 780
QY 781 ATGCAAGAGCGCATTAAGCAACTTATCGAGATTGGACCGGGGAAAGTCTTGTGAGGT 840
Db 781 TTAGTAAAGAGTGGCATAACACAACTTCAITGAGGTAGGACAGGTAAAGTTTGTGAGGT 840
QY 841 TTGTTTAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGATTTA 900
Db 841 TTGTTGAGAAATTTGATTAATAATTTACTATGACTAGTGTGAAACATGTTAGACTTTA 900
QY 901 GTAGCACTTTTAGAAAAATAG 921
Db 901 CGTTTATTTTAGTAGAGAG 921

RESULT 4

US-10-369-493-42057
; Sequence 42057, Application US/10369493
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 42057
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Lactococcus lactis
US-10-369-493-42057

Query Match 42.2%; Score 388.8; DB 8; Length 927;
Best Local Similarity 64.6%; Pred. No. 7.3e-109;
Matches 598; Conservative 0; Mismatches 322; Indels 6; Gaps 1;
QY 1 ATGACTAAACAGCGCTTTTATTGCTGGTCAAGGTGCCAGTATCTAGGATGGACGG 60
Db 1 ATGACTAAACAGCACTTTTATCTCAGTCAAGGGCACAAAAGCTTGAATGGCACT 60
QY 61 GATTTCTATGATCAGTATCCGATTGTCAAAGAAACGATTGATCGAGGAGTCAAGGTGCTC 120
Db 61 GACTTATATGACCAATATGAAACAGTTAAAGCAACTTTTGTATGAAGCAAGTCAAGCTTTA 120
QY 121 GGTATGATTTACGTTATCTCATGATACGGAAGAGACAACTCAATCAGACCCGCTAT 180
Db 121 GGATATGATTGGAGCTTTGATTGATATGATGAGAAATACTAATGAACAAAGTAC 180
QY 181 ACGAACACAGCACTTCTAGGACCTCGGTTGCTATCTACCGTTTATGCAAGAAAGGCG 240
Db 181 ACTCAACCTGCAATTTTAAACAACTGTTGCTATTTTACGTTTGTAAAGTGAAGATGG 240
QY 241 TATCAGCGCTGATGTTGCTGTTGCTCTTGGAGAACTCTGCTTGGTGGCAAGC 300
Db 241 ATTAACCTGACCTGTGTGCTGGTCTAGTCTTGGTGAATATTTCTGCTTGGTAGCATCA 300
QY 301 GGCCCTTGGATTTTGAAGATGCGGTTGCTTGGTAGCTAAGCGTGGAGCTATATGGAA 360
Db 301 GGAATCATGATTTTCAAGAGCAGTTTAACTTGTAGCTAAACGTTGCTCAATATATGACA 360
QY 361 GAACGGCTCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATAGCGCAGTAGAGTTC 420
Db 361 GAAGCTGCACCGACTGTTCTGTGTAATGCTGCTGTATGAAACACAGACCCAGCTTG 420
QY 421 ATTGAAGAAGCGCTTCAAAAAGCTTCTGAACTT-----GGAGTGGTTACTCCAGCAAC 474

Db 421 ATTGAGAAATTTCCAGAAAGCGCGGAATTTAAAGCGGTATTGTGAGTCCAGCAAT 480
QY 475 TATAACACACTGACAAATCGTCACTTCTGGAGAGTGGTTCAGATTGATCGAGCGGTT 534
Db 481 TATAACACCGCCGACAAATTTGTTTATGGTGGTGAAGTTGAGGCGGTGATTATGCTGTT 540
QY 535 GAACTTTTGAAGAGCAGGTGCCAAACGCTTGATTCTCTTAAGGTGTGAGGTCCCTTT 594
Db 541 GAGTTGCTAAAGAGCGCGAGTTTCGTAACCTTATTGAATTTAAAGTTTCAGGACCTTTC 600
QY 595 CACACCGCTCTCTTGGAGCTGTAGCCAGAACTAGCTGAAACTCTAGCTCAGGTAACT 654
Db 601 CATACAGCAATTTTAAACCCAGCATCTGAAAAATTTGCTTTGGAGCTTGATAAAATTCAT 660
QY 655 TTTTCAGATTTTACTGTCCCTAGTCGCAATACAGAACTGCTGTGATGCAGAAAGAG 714
Db 661 TTTAGACCTTTTGAATTAACCATTAATCTCAATACGAGTGTCTAAAGTAATGGAATGAT 720
QY 715 GACATGCTCAGCTCTTGAACGCTCAGGTCAAGGAACCGGTTCTGTTCTATGAAAGTATT 774
Db 721 GAAGTCAAGGACCTTTTGAACGCTCAAGTCAATGGAACAGTTCGTTTATGAAATCGGTT 780
QY 775 GGGGTCTATGCAAGAGCAGGCATTAAGCAACTTTATCGAGATTGACCGGGGAAAGTCTTG 834
Db 781 GAAACATGCAAAAACCTAGGGCGACTCGCTTTATTGAAGTGTGCTCTGGAGAGTACTT 840
QY 835 TCAGGTTTGTAAAAAATGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCG 894
Db 841 TCAGGTTTCAATAAAAAATGATAAAAAATGCAGAAATTCGTAATGTTGAAAAATTTAGCT 900
QY 895 AGTTAGTAGCACCTTTTAGAAAAATA 920
Db 901 TCATTTGAAGCTTTGATTAATCAGTA 926

RESULT 5

US-10-282-122A-20712
; Sequence 20712, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITPA 034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636

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; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20712
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-282-122A-20712

Query Match      38.1%; Score 350.8; DB 9; Length 927;
Best Local Similarity 61.7%; Pred. No. 3.8e-97;
Matches 559; Conservative 0; Mismatches 347; Indels 0; Gaps 0;

QY 7 AAACAGCCTTTTATTTGCTGTCAGAGTCCCGAGTATCTAGGATGGACGGGATTC 66
Db      |||||
QY 4 AAACAGCGATTTTATTTAGTGACAGAGAGCCAGTATCAAGGGATGGTGAAGAATTA 63
Db      |||||
QY 67 TATGATCAGTATCCGATTGTCAGAGAACGATTGATCGAGCGAGTCAGGTGCTCGTTAT 126
Db      |||||
QY 64 TATCACCAGAGCGGATTTGCGGAAACCTTTGATGAAGCAAGTCATATCTTAGTTAT 123
Db      |||||
QY 127 GATTTAGCTTATCTATCGATCGGAGAGACAAACTCAATCAGACCCGCTATACGCAA 186
Db      |||||
QY 124 GAGATGCGAGAACTTTGTTTACTGAAATGAACGTTTAAATCAACAGAAATATACGCAA 183
Db      |||||
QY 187 CCAGCCATCTAGCGATTCGGTTGCTATCTACGGTTTATGCAAGAAAGGCTATCAG 246
Db      |||||
QY 184 CCTGCTATTTAAAGTATGATGCTGCGATTTTACCGCTTTTGCAACAAAGGACTAACG 243
Db      |||||
QY 247 CCTGATATGTTGCTGTTGCTCTCTTTGGAGAACTACTCTGCCCTTGGTGGCAAGCGCGC 306
Db      |||||
QY 244 CCTGATGCTGAGCGGTTTAAAGCTTAGGGGAATACAGTCTTTGTTGCGACGGGCT 303
Db      |||||
QY 307 TTGATTTTGAAGATGGGTTGCTTGGTAGCTTAAGCGTGGAGCCTATATGGAAGAGCG 366
Db      |||||
QY 304 TTGCGCTTTTCAAGACAGTGGCGCTTGGTCCAAAGCGCGGTGAGTACATGACAGAAGCA 363
Db      |||||
QY 367 GCTCCTGCTGACTCTGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTCAATTGAA 426
Db      |||||
QY 364 GCACCAAGAACTGCAAAATGTTGCTGTTATGAATGCTGAGCGTGAAGTAATTGAG 423
Db      |||||
QY 427 GAAGCCTGTCAAAAGCTTCTGAACCTTGGAGTGGTTACTCCAGCCAACTATACACACCT 486
Db      |||||
QY 424 AAAGCCTGCCAAGAACGAGTGTCTTTCGGAATTTGCGCTCCAGCAAAATATATATACACCA 483
Db      |||||
QY 487 GCACAAATCGTCAATGCTGAGAGAGTGTGCAAGTTGATCGAGCGGTTGAACCTTTTGCAG 546
Db      |||||
QY 484 CAACAAATCGTGATGTTGAGGTTGCTGCTGTTGATCAAGCATGACACTTCTCAA 543
Db      |||||
QY 547 GAAGCAGTGCACAAAGCTTGAATTCCTCTTAAGGTGTAGGTCCCTTTTCAACCGCTCTC 606
Db      |||||
QY 544 GAAGCTGGTGAAGCGAATGATTCGCTTAAATGTAGTGGCCCTTTCCATACGGCGCTG 603
Db      |||||
QY 507 CTTGAGCTGCTGACCAAGAACTAGCTGAACCTCTAGCTCAGTGAAGTTTTCAGATTTT 666
Db      |||||
QY 604 TTACACAGCATCAAAAAATTTGGCTCAGGATTTAGCAAAATGAACTTTTCAACGATG 663
Db      |||||
QY 667 ACTTGTCCCTTAGTCGGCAATACAGAAGCTGCTGTGATGCAAAAGAGGACATTTGCTCAG 726
Db      |||||
QY 664 CAATTTCTGTCTATTAGTATACAGCTGCCGAAATTTATGCCCAAGAGGCAATTCAGCG 723
Db      |||||
QY 727 CTCTTGAGCGGTGAGTCAAGGAACCGCTTTCGTTTCTATGAAAGTATTTGGGTCATGCAA 786
Db      |||||
QY 724 TTATTGGAAGAGCAAGTCAATGCTGCGGTAGCTTTTGAAGACAGTATCGAAACGATGAAG 783
Db      |||||
QY 787 GAAGCAGGCATTAAGCAACTTATCGAGATTGGACCGGGGAAAGTCTTTGTCAAGGTTTGT 846
Db      |||||
QY 784 GCTATGACGCTAGGAACGATGATTGAAGTTGGTCCAGGGGAAACATTAATTAATGTTT 843
Db      |||||
QY 847 AAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTTAGTACGA 906
Db      |||||
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Db 844 AAAAAAATTGACAAACAAATTTGAATGCACCGTGTGAAGATGTTGCAACATTAACGAA 903
QY 907 CTTTITA 912
Db 904 ACGTTA 909

RESULT 6
US-09-134-000C-1582
; Sequence 1582, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1582
; LENGTH: 948
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1582

Query Match      38.1%; Score 350.8; DB 6; Length 948;
Best Local Similarity 61.7%; Pred. No. 3.8e-97;
Matches 559; Conservative 0; Mismatches 347; Indels 0; Gaps 0;

QY 7 AAACAGCCTTTTATTTGCTGTCAGAGTCCCGAGTATCTAGGATGGACGGGATTC 66
Db      |||||
QY 22 AAACAGCGATTTTATTTAGTGGAACAGGAGCCAGTATCAAGGGATGGTGAAGAATTA 81
Db      |||||
QY 67 TATGATCAGTATCCGATTGTCAGAGAACGATTGATCGAGCGAGTCAGGTCTCGTTAT 126
Db      |||||
QY 82 TATCACCAGAGAGCGATTTGCGGAAACCTTTGCGATGAAGCAAGTCATATCTTAGTTAT 141
Db      |||||
QY 127 GATTTACGTTTCTCATCGATACGAGAACAGCAAACTCAATCAGACCCGCTATACGCAA 186
Db      |||||
QY 142 GAGATGGCAGAACTTTGTTTACTGAAATGAACGTTTAAATGAACAGAAATATACGCAA 201
Db      |||||
QY 187 CAGCCTTCTAGGAGCTTCGTTGCTATCTACGCTTTATTTGCAAGAAAGGCTATCAG 246
Db      |||||
QY 202 CTTGCTATTTTAAACAGTCAAGTGTGCGATTTTACCGTCTTTTGCACAAAGGACTAACG 261
Db      |||||
QY 247 CTTGATATGTTGCTGTTGCTTCTCTTGGAGAACTCTGCTTGGTGGCAAGCGCGCC 306
Db      |||||
QY 262 CTTGATGCTGAGCGGTTTAAAGCTTAGGGAAATACAGTGTGTTTGGTTCAGCGGGCT 321
Db      |||||
QY 307 TTGATTTTGAAGATGCGGTTGCTTGGTAGCTAAGCGTGGAGCCTATATGGAAGAGCG 366
Db      |||||
QY 322 TTGCGCTTTTCAAGAGCAGTGGCTTGGTCCAAAAGCGCGCTCAGTACATGACAGAGCA 381
Db      |||||
QY 367 CTTCTGCTGCTACTCTGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTCAATTCAA 426
Db      |||||
QY 382 GCACCAAGAGACTGGCAAAATGTTGCTGTTTGAATGCTGAGCGTGAAGTAATTGAG 441
Db      |||||
QY 427 GAAGCCTGTCAAAAAGCTTCTGAACCTTGGAGTGGTTACTCCAGCCAACTATAACACACT 486
Db      |||||
QY 442 AAAGCTGCCAAGAGAGCCAGTCTTTTCGAAATTTGGCTCCAGCAAAATATAATACCA 501
Db      |||||
QY 487 GCACAAATCGTCAATGCTGGAGAGTGGTTGACGTTGATCGAGCGGTTGAATTTTGCAA 546
Db      |||||
QY 502 CAACAAATCGGATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 561
Db      |||||
QY 547 GAAGCAGGTGCAAAAGCTTGAATTCCTCTTAAGGTGTGAGGTCCCTTTTCAACCGCTCTC 606
Db      |||||
QY 562 GAAGCTGGTGTGAAGCGAATGATTTCCGTTAAATGTGAGTGGCCCTTTTCCATACGCGCTG 621
Db      |||||
QY 607 CTTGAGCTGTGAGCCAGAAACTAGCTGAAACTCTAGCTCAGGTAAGTTTTTCAGATTTT 666
Db      |||||
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Db 622 TTACACACGATCAAAAAATGGCTCAGATTAGCAAAATGAACCTTCAAAACGATG 681
QY 667 ACTTGTCCCTAGTCGGCAATACAGAAGCTGTGTGATGCAAAAAAGAGACATTCCTCAG 726
Db 682 CAAATTCCTGTCTATTAGTAATACGACTGCGGAATATATGCCCAAGAGCAATCAACGC 741
QY 727 CTCTTGACCGCTCAGGTCAAGAAACCGTTCTGTTTCTATGAAGATTATGGGGTCAATGCAA 786
Db 742 TTATTGGAAAGCAAGTCTGCTCGGTAACCTTTTGAAGACAGTATCGAAACGATGAAG 801
QY 787 GAAGCAGGCGATAAGCAACTTTATCGAGATTGACCGGGGAAAGTCTTCTCAGGTTTGT 846
Db 802 GCTATGAAGTAGGACGATGATTGAAGTTGTCCAGGGAAACATTAACTGGTTTGT 861
QY 847 AAAAAAATTGATCAAACTGCTCACTTACCTGCTATGTTGGAAGATCAAGCAGATTTAGTAGCA 906
Db 862 AAAAAAATTGACAAAACAAATGAAATGCACCGTGTGGAAGATGTTGCAACATTAACAGAA 921
QY 907 CTTTAA 912
Db 922 ACGTTA 927

RESULT 7

US-09-134-000C-1582
; Sequence 1582, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1582
; LENGTH: 948
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1582

Query Match 38.1%; Score 350.8; DB 6; Length 948;
Best Local Similarity 61.7%; Pred. No. 3.8e-97;
Matches 559; Conservative 0; Mismatches 347; Indels 0; Gaps 0;
QY 7 AAAACAGCGCTTTTATTGCTGGTCAAGTGCCCAAGTATCTAGGGATGGGACGGGATTC 66
Db 22 AAAACAGCGATTTTATTAGTGGAACAAGAGGCCAGTATCAAGGATGGTGAAGATTA 81
QY 67 TAGATCAGTATCCGATTTGTCAAAAGAAAGATTGATCGAGCGAGTCAGTCTCGTTAT 126
Db 82 TATCACCAGAGCGGATTTGTCGGAAACTTTTCGATGAAGCAAGTCATCTTAGGTTAT 141
QY 127 GATTACGTTATCTCATGATACGGAAGAGCAAACTCAATCAGACCGCTATACGCAA 186
Db 142 GAGATGGCAAGACTTTGTTTACTGAAATGAACTGAAATGAAACAGATATACGCAA 201
QY 187 CGAGCCATTCAGGACTTCGGTTGCTATCTACCGTTTATTCGAAAGAAAGGCTATCAG 246
Db 202 CCGTCTATTTAACAGTCAGTCTGCATTTTACCCTCTTTTGCACAAAAAGGACTAACG 261
QY 247 CCGTATATGTTGCTGGTTTGTCTCTTGAGAAATCTGCTTGGTGGCAAGCGGGCC 306
Db 262 CCGTATGTCGTAAGCGGTTTAACTTAGGGAATACAGTCTGTTGGTTCAGCGGGCT 321
QY 307 TTGGATTTTGAAGATTCGGGTTCCCTTGGTAGCTAAGCGTGGAGCCTATATGGAAGAGCG 366
Db 322 TTGCGCTTTTCAAGAGCAGTGGCTTTGTTCCAAAAGCGGTCAGTACATCACAGAAGCA 381
QY 367 GCTCCTGCTGACTCTGGCAAGATGATAGCAGTTCTCAATACCGCAGTAGAGTTCATGAA 426

Db 382 GCACCAAGGAACTGCAAAATGGTTGCTTATGAATGCTGAGCGTGAAGTAAATTGAG 441
QY 427 GAAGCCCTGTCAAAAGCTTCTGAACCTGGAGTGGTTACTCCAGCCAACTATACACACCT 486
Db 442 AAGCCTGCCAAGAACGAGTCTTTTCGGAATTTGGCTCCAGCAATTTATATACCA 501
QY 487 GCACAAATGCTCATTCTGAGAGAGTGGTTGAGTTGATCGAGCGGTTGAACCTTTTGCAA 546
Db 502 CAACAAATGCTGATTGGTGGTGGTGTCTGCTGTTGATCAAGCGGATGACACTTCTCAA 561
QY 547 GAAGCAGGTGCCAAACGCTTTCCTCTTAAGGTGTGAGTCCCTTTTCCACACCGCTCTC 606
Db 562 GAAGCTGGTGTGAGAGCAATGATTCGTTAAATGTTGAGTGGCCCTTCCATACGGGCTG 621
QY 607 CTTGAGCCCTGTAGCCAGAAACTAGCTGAAACTCTAGCTCAGGTAAAGTTTTCAGATTTT 666
Db 622 TTAACAACAGCATCAAAAAAATGGCTCAGGATTTAGCAAAATTTGAACCGATG 681
QY 667 ACTTGTCCCTAGTCGGCAATACAGAAAGCTGTGTGATCAAAAAAGAGACATTTGCTCAG 726
Db 682 CAAATTCCTGCTCATTAATAGTACTGCGGAAATTTATGCCCAAGAGCAATTCAGCG 741
QY 727 CTCTTGACCGCTCAGGTCAAGGAAACCCGTTCTGTTCTATGAAAGTATTTGGGTCAATGCAA 786
Db 742 TTATTGAAAAAGCAAGTCTGTCTGCGTACGTTTGAAGACAGTATCGAAACGATGAAG 801
QY 787 GAAGCAGGCGATAGCAACTTTATCGAGATTGGACCGGGGAAAGTCTTGTCAAGTTTGT 846
Db 802 GCTATGAAGTAGGACGATGATTGAAGTTGTTCAGGGAAACATTAACTGTTTGT 861
QY 847 AAAAAAATTGATCAAACTGCTCACTTACCTATGCTATGGAAGATCAAGCGGATTTAGTAGCA 906
Db 862 AAAAAAATTGACAAAACAAATGAAATGCACCGTGTGGAAGATGTTGCAACATTAACAGAA 921
QY 907 CTTTAA 912
Db 922 ACGTTA 927

RESULT 8

US-10-434-665-1582
; Sequence 1582, Application US/10434665
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: PAT03-09
; CURRENT APPLICATION NUMBER: US/10/434,665
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: US 09/134,000
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1582
; LENGTH: 948
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-434-665-1582

Query Match 38.1%; Score 350.8; DB 8; Length 948;
Best Local Similarity 61.7%; Pred. No. 3.8e-97;
Matches 559; Conservative 0; Mismatches 347; Indels 0; Gaps 0;
QY 7 AAAACAGCGCTTTTATTGCTGGTCAAGTGCCCAAGTATCTAGGGATGGGACGGGATTC 66
Db 22 AAAACAGCGATTTTATTAGTGGAACAAGAGGCCAGTATCAAGGATGGTGAAGATTA 81
QY 67 TAGATCAGTATCCGATTTGTCAAAAGAAAGATTGATCGAGCGAGTCAGTCTCGTTAT 126
Db 82 TATCACCAGAGCGGATTTGTCGGAACTTTTCGATGAAGCAAGTTCATATCTTAGTTAT 141

127 GATTACGTTATCTCATCGATACGAGAGACAAACCTCAATCAGACCGCTATACGAA 186
 142 GAGATGGCAGAACCTTTTACTGAAATGAACGTTAAATGAAACAGATATACGAA 201
 187 CAGCATTCTAGCAGACTCGGTGCTATCTACGTTTATGGAAGAAAGGGCTATCAG 246
 202 CCTGCTATTTAAACAGTCAAGTGCAGCTTTTACCGTCTTTTGCACAAAGAAAGGACTAAG 261
 247 CTTGATATGGTGTCTGCTTCTGGAATATCTCTGCTTGGTGGCAAGCGGCGCC 306
 262 CTTGATGCTGAGCGGTTTAAAGCTTAGGGAATACAGTGTGTTGGTTCAGCGGGCT 321
 307 TTGGATTTGAAGATGCGGTTGCTTGTAGTCAAGCGTGAAGCTATATGAAGAAGCG 366
 322 TTGGCTTTTTCAGAGCAGTGCCTTGGTCAAAAGCGCGTCAATGATGACAGAAAGCA 381
 367 GCTCCTGCTGACTCTGCAAGATGATAGCTTCTCAATAGCCAGTAGAGTCAATGAA 426
 382 GCACACAAAGAACTGGCAAAATGTTGCTGTTATGAATGCTGAGCGTGAAGTAAATGAG 441
 427 GAAGCTCTCAAAAGCTTCTGAATTTGGAGTGGTTACTCCAGGCAACTATAACACACCT 486
 442 AAAGCTGCCAAGAACCGAGTCTTTCGAATTTGGCTCCAGCAAAATTAATATACACCA 501
 487 GCACAAATCGTATCTGCTGGAGAAAGTGTTCAGTTCAGTTCAGCGGTGAACTTTGCAA 546
 502 CAACAAATCGTATTTGGTGGAGTGTCTGCTGTTGATCAAGCGATGACACTTCTCAA 561
 547 GAAGCAGGTGCCAAACGCTTGTATCTTAAAGTGTGAGTCCCTTTTCACACCGCTCTC 606
 562 GAAGCTGGTGTCAAGCGAATGATTCGGTTAAATGAGTGGCCCTTTCCATACGGCGCTG 621
 607 CTTGAGCTGTAGCCAGAACTAGCTGAAACTCTAGCTAGGTAAGTCTTTCAGATTTT 666
 622 TTACAAACAGCTCAAAATAATGCTCAGGATTTAGCAAAATGAACTTTTCAACGATG 681
 667 ACTTGTCCCTAGTCCGCAATACAGAGCTGCTGTGATGCAAAAGAGGACATTTGCTCAG 726
 682 CAATTCCTGTCTATGATTAACAGCTGCCGAATTAATGCTCCAGAGGCAATCAAGCG 741
 727 CTTTTCAGCGCTAGGTCAGGCAAGAACCGCTTCTGTTCTATGAAGATTTGGGCTCATGCA 786
 742 TATTGGAAGAGCAAGTCACTGCTGCGGTAGCTTTTGAAGACAGATATCGAAACGATGAAG 801
 787 GAAGCAGCATAGCAACTTTATCGAGATTCGACCGGGAAGTCTTCTCAGGTTTGT 846
 802 GCTATGAACGTAGGAAACGATGATTAAGTGTGCTCAGGGAACCAATTAACCTGTTTGT 861
 847 AAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTTAGTAGCA 906
 862 AAAAAAATTGACAAAACAAATTGAAATGCAACCGTGTGGAAGATGTTGCAACATTAACAGAA 921
 907 CTTTGA 912
 922 ACGTTA 927

RESULT 9

US-10-282-122A-21491
 ; Sequence 21491, Application US/10282122A
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.

APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA 034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 21491
 LENGTH: 915
 TYPE: DNA
 ORGANISM: Enterococcus faecium
 US-10-282-122A-21491

Query Match 34.4%; Score 316.8; DB 9; Length 915;
 Best Local Similarity 60.0%; Pred. No. 1.1e-86;
 Matches 547; Conservative 0; Mismatches 362; Indels 3; Gaps 1;
 QY 7 AAAAAAGCCTTTTATTTCTGCTGTCAGGTGCCAGTATCTAGGATGGACGGGATTTTC 66
 Db 4 AAAAAAGCCTTTTATTTCTGCTGTCAGGTGCCAGTATCTAGGATGGACGGGATTTTC 63
 QY 67 TATGATCAGTATCCGATTTGTCAGGATGTCAGGATGTCAGGATGTCAGGATGTCAGGAT 126
 Db 64 TATGAAGAAG---CCGTTGTAAGCAGACATTTGATGAAGCAAGTCAGATTTCTCGGCTAC 120
 QY 127 GATTTACGTTATCTCATCGATAGGAGAGACAACTCAATCAGACCGCTATACGAA 186
 Db 121 GATATGGCTGAACCTTTGCTTTACAGAAATGAACGTTGGATCAGACGCAATATACACAG 180
 QY 187 CCAGCCATTTCTAGCGACTTCGGTTGCTATCTACCTGTTTATTGCAAGAAAGGGCTATCAG 246
 Db 181 CCAGCTATTTCTACAGTCAGATCGGTATTTATCGCTTATTGAAGGAGCATGGAATCATC 240
 QY 247 CTTGATATGTTGCTGTTGTTGCTCTTGGAGAAATCTCTGCTTGGTGGCAAGCGGCGCC 306
 Db 241 CCAGATGCACTTTTAGGACTGAGTTTAGGAGAATATTCCGCAATTAGTAGTATGATGCG 300
 QY 307 TTGGATTTTGAAGATGCGGTTGCTTGGTGTAGCTAAGCGTGGAGCGCTATATGGAAGAAGCG 366
 Db 301 CTATCTTCTCAGTGAAGCAGTTCGGTTAGTGAAGAAAGGCGCTTATATGACAGAGCT 360
 QY 367 GTCCTGCTGACTCTGGCAAGATGTTAGCAGTTCTCAATACGCCAGTAGAGTCAATGAA 426
 Db 361 GCCCCAGCTGGAAGCGGGGAAATGTTGCAATGATGAATGCAATGCAATGCAATGCAATGCA 420
 QY 427 GAAGCCTGTCAAAAGCTTCTGAACCTTGGAGTGGTTACTCCAGGCAACTATATACACACCT 486
 Db 421 GAAAGCTGTCTGAAGCTAGCAAGTACGGCATCGTATCTCTGCAATTTATATACACCT 480
 QY 487 GCACAAATCGTCAATTTGCTGGAGAAGTGTGTCAGTTGATCGAGCGGTTGAACTTTTGA 546
 Db 481 CAGCAGATCGTATGTTGGTGGCAAGAAAGGAGGAGTAGACGAAGCTGTTTACTATTAAAA 540

QY 547 GAAGAGGTCGCAACGCTTGATCTCTTAAGGTGTCAGTCCCTTTTACACCGCTCTC 606
Db 541 GAAAGAGGTTCAAAAGAAATGATCCCTCTAAATGTGACGGGCTTTTCATACAGCTATT 600
QY 607 CTTGAGCCTGCTAGCGAGAACTAGCTGAACTCTAGCTCAGTAAAGTTTTCAGATTTT 666
Db 601 TTAGAACCGGCGCAAAAATCTGGGAGGACCTTAAGTCAGATCAATCTCTGAACCT 660
QY 667 ACTTGTCCTCTAGTCGGCAATACAGAACTGCTGTGATGCAAAAAGAGAGACATCTCTCAG 726
Db 661 TCTTTTCTCTATCATAGCAACACCAACCGGAAATTAATGAAGAAAGAAACCAATCGCGGA 720
QY 727 CTCTTGACCGCTCAGTCAAGAACCCGTTCTGTTCTATGAAGATTTGGGTCATGCA 786
Db 721 CTACTTGACAGCAAGTCATGCAACCTGTTCTGTTCTATGAGAGTATCCATAGTTAAA 780
QY 787 GAAGCAGGATAGCAACTTTATCGAGATTTGACCGGGGAAAGTCTTGTGAGTTTGT 846
Db 781 ACAATCGGATCGAACAGTCTGAAAGTCGGCCCGGAAAGTATTAAGCGGATTTATG 840
QY 847 AAAAAAATGATCAACTGCTCCTACCTAGCTCATGTGGAAGATCAAGCGAGTTTAGTAGCA 906
Db 841 AAAAAAATGATCAACTGCTCCTACCTAGCTCATGTGGAAGATCAAGCGAGTTTAGTAGCA 900
QY 907 CTTTGAAGAAA 918
Db 901 ACAATAGCAATA 912

RESULT 10

US-10-417-884-3319
; Sequence 3319, Application US/10417884
; GENERAL INFORMATION:
; APPLICANT: Lynn A. Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; ;
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/417,884
; FILING DATE: 17-Apr-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3319:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 987 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...987
SEQUENCE DESCRIPTION: SEQ ID NO: 3319:
US-10-417-884-3319

Query Match 34.2%; Score 315.2; DB 8; Length 987;
Best Local Similarity 59.9%; Pred. No. 3,7e-86;
Matches 546; Conservative 0; Mismatches 363; Indels 3; Gaps 1;
QY 7 AAACAGCCTTTTATTTGCTGTCAGGTGCCAGTATCTAGGGATGGACGGGATTTT 66
Db 73 AAACAGCATTCTTATTTAGTGCCCAAGGTGCAATATCAAGGTATGGGAAAGATTTA 132
QY 67 TATGATCAGTATCCGATTGTCAAAGAAAGATTGATCGAGCGAGTCAGGTGCTCGGTAT 126
Db 133 TATGAGAAG--CCGTTGTAAGACAGACATTTGATGAAGCAAGTCAGATTCTCGGCTAC 189
QY 127 GATTAGCTTATCTATCGATACGGAAGAGACAACTCAATCAGACCCGCTATACGCAA 186
Db 190 GATATGGCTGCACTTTGCTTTACAGAAAATGAACGTTTGGATCAGACGCAATATACACAG 249
QY 187 CCAGCCATCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAGGGCTATCAG 246
Db 250 CCAGCTATTCTACAGTCAGCATCGGTATTATCGCTTATTGAAGGAGCATGGAATCATC 309
QY 247 CTGATATGTTGCTGTTTGTCTCTTTGAGAAATATCTGCTTGGTGGCAAGCGGCGCC 306
Db 310 CCAGATGCACTTTAGGACTGAGTTAGGAGAAATATTCGGCATTAGTAGCTAATATGCG 369
QY 307 TTGATTTTCAAGATCGGTTGCTTTGAGTGAAGCTGAGCGCTATATGGAAGAGCG 366
Db 370 CTATCTTCACTGAAGCAGTTGGTTAGTAGCAAAAAGAGGCGCTTATATGACAGAAGCT 429
QY 367 GCTCTGCTGACTCTGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTCAATTGAA 426
Db 430 ACCCAGCTGGAAGCGGGAATATGGTTGAGTGAATGATGATGCGCGGATTGAAACGATCGAG 489
QY 427 GAAGCCTGTCAAAAAGCTTCTGAACITGGAGTGGTTACTCCAGCCCACTATAACACACT 486
Db 490 GAAAGCTGTCTGAAGCTAGCAAGTAGGCTATCTCTCTGCAATATTAATACACT 549
QY 487 GCACAAATCGTCTATGCTGGAAGTGGTTGAGTTGATCGAGCGGTGTAACCTTTTGCAA 546
Db 550 CAGCAGATCGTATTTGGTGGCAAGAAAGAGCAGTAGACGAAGCTGTTTACTATTAAAA 609
QY 547 GAAGCAGTGCACAAACGCTTGATTCTCTTAAGGTGTAGGTCCCTTTTACACCGCTCTC 606
Db 610 GAAAAGGTTTCAAAAGAAATGATCCCTCTAAATGTGACGGGCTTTTCTACAGCTATT 659
QY 607 CTTGAGCCTGCTAGCCAGAACTAGCTGAAACTCTAGCTCAGGTAAGTTTTCAGATTTT 666
Db 670 TTAGAACCGGCGCAAAAATCTGGGAGGACCTAAGTCAGATTCAATCTCTGAACCT 729
QY 667 ACTTGTCCTCTAGTCGGCAATACAGAACTGCTGTGATGCAAAAAGAGACATGTCTCAG 726
Db 730 TCTTTTCTCTATCATAGCAACCAACCGGAAATTAATGAAGAAAGAAACCAATCGCGGGA 789
QY 727 CTCTTGACCGCTCAGGTCAAGGAACCGGTTCTGTTTCTATGAAAGTATTTGGGTCATGCAA 786
Db 790 CTACTTGAACAGCAAGTCATGCAACCTGTTCTGTTTCTAGAGAGTATCCATAGTTAAAA 849
QY 787 GAAGCAGCATAGCAACTTTATCGAGATTTGACCGGGGAAAGTCTTGTGAGGTTTGT 846
Db 850 ACAATCGGCTCGAACCAAGTCATCGAAGTCGGGCGGAAAGTATTAAGCGGATTTATG 909
QY 847 AAAAAAATGATCAACTGCTCCTACTAGCTCATGTGGAAGATCAAGCGAGTTTAGTAGCA 906

Db 910 AAAAAATCGATAAAACAATACCAGTTCTCGGTGTGAGATAAGCAGACATTGTATGAA 969
QY 907 CTTTGTAGAAAA 918
Db 970 ACAATAGCAATA 981

RESULT 11
US-10-282-122A-41191
; Sequence 41191, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41191
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Vibrio cholerae
US-10-282-122A-41191

Query Match 23.6%; Score 217.6; DB 9; Length 939;
Best Local Similarity 55.5%; Pred. No. 4.3e-56;
Matches 484; Conservative 0; Mismatches 379; Indels 9; Gaps 3;

QY 1 ATGACTAAAACAGCGCTTTTATTTGCTGTGTCAGGTGCCAGTATCTAGGGATGGGACGG 60
Db 16 ATGAGTAAGTTTGCTATCTATTTCCAGGTCCAGGCTCGCAAGCAGTAGGTATGCTGGCT 75
QY 61 GATTTCATGATCAGTATCCGATGTCNAAAGAACGATTGATCGAGGAGTCAGGTGCTC 120
Db 76 GACCTTGGCGAGCAGTATGCTGTGTGTAATAAACAACATTCGCCGAGGTTCTCAGAGTGCCT 135
QY 121 GGTATGATTTACGTTATCTCATC---GATACGGAAGAGACAAACTCAATCAGACCCGC 177
Db 136 GGTACGATCTCTGGCCCTGGTTCAGATGCGCCCTGTGGAAGATCTCAACCAACTTTC 195
QY 178 TATACGCAACAGCCCAATCTAGCGACTTCGGTGTGCTATCTACCGGTTTATTGCAAGAAAG 237

Db 196 CGTACTCAACCTGCGTTGCTTGCCTCTGTTGGGATTTGGCGTGTATGGCAGCACTG 255
QY 238 GG---CTATCAGCCTGATATGCTGCTGCTTGTCTCTTTGGAGAAATATCTCTCCCTTGGTG 294
Db 256 GGTCTTTGAGCAACCTGCGGTTTTAGCTGCTCACAGCTTGGGTGAATATTCAGCACTGGTA 315
QY 295 GCAAGCGGCGCTTGGATTTTGAAGATCGGTTGCTTGGTGTAGCTAAGCGTGGAGCCTAT 354
Db 316 TGTGCGGCGCTGATTGATTTTAAACAAGGATCAAGCTGGTTGAGCTGGTGGTCAATG 375
QY 355 ATGGAAGAAGCGCTCTCTGCTGACTCTGCGCAAGATGGTAGCAGTTCTCAATACGCCAGTA 414
Db 376 ATGCAACAGCGGTGCTGCGGTACGGGTCAATGTACGCGATCATCGTCTAGAAGAT 435
QY 415 GAGGTCAATTGAAGAGCGCTGTCAAAAGCTTCTGAACTTGGAGTGGTACTCCAGCCAC 474
Db 436 GAAGCGATTGCTAAAGCCTGCTGACGCGGCGAAGGTGAAGTGGTCTCTCTCTTAAC 495
QY 475 TATAACACACCTGTCACAAATCGTCTGCTGGAGAGTGGTTGCAAGTTGATCGAGCGGT 534
Db 496 TTTAACTCACCAGGCCAAGTGGTTATTGCTGCTCAAAAAGATGCGGTTGAGCGTGGCGGC 555
QY 535 GAACCTTTTCRAGAAGCAGGTGTCRAGACCTTGATTCCTCTTAAGTGTGTCAGTCCCTTT 594
Db 556 GTTCTGTGTAAGAAGCGGCGCGAAGCTGCGCTCTGCCAGTTTCCGTACCATCA 615
QY 595 CACACCGCTCTCTGAGCCTCTAGCCAGAACTAGCTGAAACTCTAGCTCAGGTAAAGT 654
Db 616 CACTGCGGTTGATGAAGCTGCTGCCGATGAATTGGCAAAACTCTAGCAGAGCTTGA 675
QY 655 TTTTCAGATTTTACTTGTCCCTCTAGTCCGCAATCAGAAAGCT---GCTGTGATGCAAAA 711
Db 676 TTCAATGCAACCAAAATTCGGTCTCATCAATAACGTTGATTTGTGGCTGAAACCGATCCG 735
QY 712 GAGGACATTTGCTCAGCTCTTGACGCTCAGGTCAAGGAACCGCTTCGTTCTATGAAAGT 771
Db 736 GTAAAAATTAAGATGCGTTGATTCGTCACCTATAGCCAGTTCTGTGGACTGAATGC 795
QY 772 ATGGGGTTCATGCAAGAAGCAGGCATTAAGCAACTTTATCGAGATTGGACCGGGGAAAGTC 831
Db 796 GTTGAACAAATGAGCGCACAGGTGTCGAAAAGCTGATTGAAATGGGCGCGGTAAAGTA 855
QY 832 TTGTCAGGTTTTGTTAAAAAATTCATCAAC 863
Db 856 TTGACTGGTCTAACAAAACGTTATTGTA AAAAC 887

RESULT 12
US-10-282-122A-32186
; Sequence 32186, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727

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; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32186
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-10-282-122A-32186

Query Match      21.3%; Score 196.4; DB 9; Length 930;
Best Local Similarity 53.0%; Pred. No. 1.5e-49;
Matches 491; Conservative 0; Mismatches 426; Indels 9; Gaps 3;

QY      1 ATGCTTAAACACGCTTTTATTTGCTGCTCAAGTGCCCATCTACTAGGATGGACGG 60
DB      1 ATGACTGATTTTCCAATGTTTCCCTGGACAGGATCAACAGCGATTGGAATGTTGCA 60

QY      61 GATTTCTATGATCAGTATCCGATTTGTCAAGAAACGATTGATCGAGCGAGTCAGGTGCTC 120
DB      61 GAACTTGGCGAGCATTTATCCATAGTGACAGAAACATTTGCTCAAGCATCTGATGATG 120

QY      121 GGTATGATTAGCTTATCTCATGATACGAA---GAAGCAAACTCAATCAGACCCGC 177
DB      121 GGTATTTCTTTTGGGATTTAGTGCAAAATGCTCTGGAAGAGAGTTAAACAAAACATGG 180

QY      178 TATACCAACACGACCATTTAGGACCTTCGGTTGTGTTATCTACCGTTTATTGCAAGAAA-- 235
DB      181 AAACACACGCGCATTTATAGCAGATCCGTTGTCTATTGCGGAGTAGTGCNAGAAAA 240

QY      236 -AGGGTATCAGCCTGATAGTTGCTGTTTGTCTCTTGGAGAAATCTCTGCTTGGTG 294
DB      241 CAAGGCAAAATGSCAAAATGATGCGAGTCAAGTCTTGGTGGAGTATCTGCTTTAGTC 300

QY      295 GCAAGCGCGCCTTGGATTTTGAAGATGCGGTTGCTTGGTAGCTAAGCGTGGACCTAT 354
DB      301 TGTGCTGGCGTAATTGATTTTGTGCGGCGATTAACCTAGTAGAATTGCGCGGTCAATTA 360

QY      355 ATGGAAGAAAGCGGCTCTCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTA 414
DB      361 ATGCAAGAGCTGTACCTCAGGTACTGCGCGCATGATGCAATATCGGATTAGATAAT 420

QY      415 GAGTCATTGAGAAGCCTGTCAAAAGCTTCTGAACCTTGGAGTGGTTACTCCAGCCAA 474
DB      421 GATGCTATTGCAAAAGCTTGTGAAGATGCGGCTCAAGGACAAGTTGTCTCACCTGTGAAC 480

QY      475 TATAACACACCTGTCAAAATCTGATTTGCTGGAGAGTGGTTGTCAGTTGATCGAGCGGTT 534
DB      481 TTTAACTACCCGCTCAAGTGGTGAATTGGGGGTATAAAGAGCGGTAGAGCGTGCAGGG 540

QY      535 GAACTTTTGAAGACAGGTGCGAAACGCTTGTATCTCTTAAAGTGTGAGTCCCTTT 594
DB      541 GCATTATGTAAGAAGCTGTGAGCGAAACGCTGCTTACCTTTAGCGGTAAAGTGTGCTTCT 600

QY      595 CACACCGCTCTCTCTGAGCCTGTAGCCAGAACTAGCTGAAACTCTAGCTCAGTAAAGT 654
DB      601 CACTGTGCTTTAATGAGCCTCTGTCAGATAGTAGTGTGCTTGTGATTCGAGAATTTGAA 660

QY      655 TTTTCAGATTTTACTTGTGCTCCCTAGTTCGCGCAATACAGAAG---CTGCTGTGATGCAAAA 711
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DB      661 TTTAAACACCTGAAATTCAGTTGTTTAATATGTTGATGTGAAGCACAAACCGATGCT 720
QY      712 GAGGACATTGCTCAGCTCTTTGACGCGTCAAGGACCCGTTGCTTTCTATGAAAGT 771
DB      721 AATGCTATTGAGATGATGATTAGTTGCTCAGCTTTATAACCCAGTCCGCTGAGTGAACG 780
QY      772 ATTGGGTCATGCAAGAGCAGGATCAAGCACTTTATCGAGATTGACCGGGGAAAGTC 831
DB      781 GTTGAATTTATTGCTGTAAGGCGCATCACAAATTTATAGAAATAGGACCGGTAAAGTA 840
QY      832 TTGTCAGGTTTGTATAAAAAAATTGATCAAACTGCTCAGCTAGCTCATGTGGAAGATCAA 891
DB      841 TTAAGTGTTTAAGGAAACGATTTTCTAAAGAGATGAACGCTGCAGCAGTTATGATATT 900
QY      892 CGAGTTTATAGCAGCTTTTAGAAAA 917
DB      901 GCATCATTAGACGCTGATTAGGAAA 926

RESULT 13
US-10-282-122A-21907
; Sequence 21907, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haseibeck, Robert
; APPLICANT: Chisen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OR INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21907
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Haemophilus influenzae
US-10-282-122A-21907

Query Match      21.3%; Score 196.4; DB 9; Length 939;
Best Local Similarity 54.1%; Pred. No. 1.5e-49;
Matches 470; Conservative 0; Mismatches 366; Indels 12; Gaps 3;
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QY	1	ATGACTAAACAGCCCTTTTATTTGCTGGTCAAGGTGCCAGTATCTTAGGATGGGACGG	50
Db	1	ATGAAAAAATTTCGAATGGTCTTCCAGGTCAAGGCTCCCAAACCTGTCGGTATGCTTGGCT	60
QY	61	GATTTCCTATGATCAGTATCCGATGTCACAAAGACGATTGATCGAGCGAGTCAAGTGCTC	120
Db	61	GATCTTGCACCTGAATATCCAATCGTTATTGAAACATTTAAACAAGCATCTGATGCGCTT	120
QY	121	GGTTATGATTACGTTATCTCATGATACGG---AAGAAGACAAACTCAATCAGACCGC	177
Db	121	GGTTATGATTATGTTATCTTGTTCAACAAGGCTCCAGTGAAGAACTTATATAAACTTGG	180
QY	178	TATACGCACACAGCCATTCTACGACATTCGGTCTCTATCTACCGTTATTTCGAGAAAG	237
Db	181	CAAACTCAGCCCGCACTTTAGCTGTTTCAGTCCGCTATTATCCGGTATGGAAGAAGAAA	240
QY	238	GGCTATC-----AGCCTGATATGGTTGCTGGTTGTCTCTTGAGAACTACTCGCTTG	291
Db	241	TTTCCCTCAATTAAACACAGAAGTATGCGACGTCATAGCTTAGTGAGTATTCTCGGTTA	300
QY	292	GTGGCAAGCGGGCCTTGGAATTTGAGATCGGTTGCTTGGTAGCTAAGCGTGAGCC	351
Db	301	GTTTGTGCTGGCGTTGGATTTCCAGATCGGATTAAATTAGTGGAAATTGCGCGGAAA	360
QY	352	TATATGGAAGACGGCTCCTGCTGACTCTGGCAAGATGTCAGCAGTCTCTCAATACGCCA	411
Db	361	TTAATGCAACAGCTGTGCTGAAGGCACCTGGCCCAATGATGCAATCATTTGGTTTAGAT	420
QY	412	GTAGAGGTCATTGAAGAGCGCTGTCAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCG	471
Db	421	AATGAAGCAATTTATTAATGCTTTGCAACACAGCAGAGGAAGCGAAAGTCGTATCTGGCGTG	480
QY	472	AACTATAACACACCTGCACAAATCGTCAATCTCTCGAGAAAGTGTTGTCAGTTGATCGAGCG	531
Db	481	AACTTTAACTCACCGGTCAGTAGTTATTGCGGGTCGGAAGCTGCAGTTAGCGTGGC	540
QY	532	GTTGAACCTTTTCAAGAAAGCGGTGCCAAACCGCTTGATTCCTCTTAAGGTGTCAAGTCCC	591
Db	541	GCTGCATTATGTAAAGAAAGCAGGGCGGAAAAGTGCAATTCGCGTTAGCTGTGAGCGTACCT	600
QY	592	TTTTCACCGCTCTCTTTGAGCGCTGTAGCCAGAAACTAGCTGAACTCTAGCTCAGCT	650
Db	601	TCTACTGTGCAATTAAAGAACTTCAGCCGAGCAATTAGCGGTAACTTTGAGATATT	660
QY	651	--AAGTTTTTCAGATTTTACTTTGCCCTAGTCGGCAATACAGAACTGCTGTGATGCAA	708
Db	661	CAAAATTAATACACCAACAATATCGGTATTAATAACGTTGATGTGAAGCTGAACTGAA	720
QY	709	AAAGAGGACATTTGCTCAGCTCTTGACGGGTCAAGTCAAGGAAACCCGTTTCGTTCTTAGAA	768
Db	721	GGCACCGAAATTCGTACCGCACTTTGTGGGTCAAGTTATATAGTCCAGTTCGTTGGACTGAA	780
QY	769	AGTATTTGGGTCATGCAAGAACGAGGCATTAAGCAACTTTATTCAGAGATTGGACCGGGAAA	828
Db	781	ACAGTTGAAAANATGGCCACAGATGGCGTTCTAGTGTCTGNAAGTGGGGCCAGGTAA	840
QY	829	GTCTGTGTCAGGTTTTGTTTAAAAAAATTG	856
Db	841	GTATTAAATGGTTTTAAACCAACGCATTG	868

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RESULT 14
US-08-487-429B-1/c
; Sequence 1, Application US/08487429B
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Frag
; TITLE OF INVENTION: Thereof, and Uses Thereof
; FILE REFERENCES: PB186P1
; CURRENT APPLICATION NUMBER: US/08/487,429B
; CURRENT FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/426,787
; PRIOR FILING DATE: 1995-04-21

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1 / NUMBER OF SEQ ID NOS: 1
2 / SOFTWARE: PatentIn version 3.1
3 / SEQ ID NO 1
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6 / ORGANISM: Haemophilus influenzae
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8 / NAME/KEY: misc_feature
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10 / OTHER INFORMATION: n equals a, t, g o r c
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69 / LOCATION: (51786)..(51786)

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OTHER INFORMATION: n equals a, t, g or c
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LOCATION: (152530)..(152530)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (152735)..(152735)
OTHER INFORMATION: n equals a, t, g or c
Query Match 21.3%; Score 196.4; DB 4; Length 1830121;
Best Local Similarity 54.1%; Pred.No. 3.9e-48; Mismatches 386; Indels 12; Gaps 3;
Matches 470; Conservative 0;
QY 1 ATGACTAAAAACAGCCCTTTTATTTGCTCAAGGTGCCAGTATCTAGGATGGACGG 60
DB 172507 ATGAAAAAATTCGAATGGTCTCCAGGTCAAGGCTCCAAACTGTCGGTATGCTTGT 172448
QY 61 GATTCTATGATCAGTATCGATTGTCAAGAAACGATTGTCGCGAGTCAGGTGCTC 120
DB 172447 GATCTTGCACACTGAATATCCAAATCGTTATTGAAACATTTAAACAAGCATCTGATGGCTT 172388
QY 121 GGTTATGATTACGTTATCTCATCGATACGG---AAGAAAGACAAACTCAATCAGACCCGC 177
DB 172387 GGTTATGATTATGGTATCTTGTCAACAGGTCAGGCTGAAGAACTTAATATAAATTGG 172328
QY 178 TATACGCAACAGCCATTCAGGACTTCGGTTGCTATCTACGTTATTGCAAGNAAG 237
DB 172327 CAAACTCAGCCCGCACTTTTAGTCGTTTATTCAGTCGTTATTTATCGGTATGGAAGAAAAA 172266
QY 238 GGCTATC-----AGGCTGATATGGTTGCTGTTTGTCTCTCTGGAGATACTCTGCTTGT 291
DB 172267 TTTCTCAATTAACCAAGAGTGATGGCAGTCATAGCTAGGTAGTATTTCTGCGTTA 172208
QY 292 GTGCAAGCGCGCCCTTGGAATTTGAAGATCGGTTGCCCTTGGTAGCTAAGCGTGAGCC 351
DB 172207 GTTTGTGCTGGCGTGTGGATTTCGAAGATGCGATTAAATTAGTGAATTGCGCGAAAA 172148

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QY 352 TATATGAAGAGGGCTCTCTGCTGACCTCTGCGCAAGATGCTAGCAGTTCTCAATACGCCA 411
Db 172147 TTAATGCAACAGCTGTCTGCTGAAGGCACTGCGCAATGATGCAATCAATTTAGAT 172088
QY 412 GTAGAGGTCATTGAAGAGCCTGTCAAAAGCTTCTGAACTTGAGTGGTGTATCCAGCC 471
Db 172087 AATGAAGCAATTAATTAATGCTTGAACAAGCAGAGGAGCGAAGTCGTATCTGCGGTG 172028
QY 472 AACTATACACACCTGTGCAAAATCGTATTCTCGAGAAGTGGTTGCGAGTTGATCGAGCG 531
Db 172027 AACTTTAACTACCGGGTCAAGTAGTTATTTCGGGGTGGCAAGCTGCAAGTTGAGCGTGG 171968
QY 532 GTTGAACCTTTGCAAGAGAGGTCGCCAAAGCTTTGATTTCTTAAAGTGTGTCAGTCC 591
Db 171967 GCTGCATTATGTAAGAAGCAGAGGCGCAAAAGCTTCATTGCGGTAGCTGTGAGCGTACCT 171908
QY 592 TTTGACACCGCTCTCTTGGCCCTGCTAGCCAGAACTAGCTGAACTCTAGCTCAGGT- 650
Db 171907 TCTCACTGTGATTAAATGAACCTGACCCAGCAATGAGCGTAACTGAGATATT 171848
QY 651 --AAGTTTTTCAGATTTTACTTGTCCCTAGTCGGCAATACAGAGCTGCTGTGANGCAA 708
Db 171847 CAATTAATACACCAACAATATCGTATTAAATAACGTTGATGTGAAAGCTGAACTGAA 171788
QY 709 AAAGAGGACATGCTCAGCTCTTGAAGGCTCAGGTCAGGCAAGGACCGTTCGTTCTATGAA 768
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RESULT 15
US-10-329-960-1/c
; Sequence 1, Application US/10329960
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Frag
; TITLE OF INVENTION: Thereof, and Uses Thereof
; FILE REFERENCE: PB186Pl
; CURRENT APPLICATION NUMBER: US/10/329,960
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: US 09/643,990
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 08/487,429
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/426,787
; PRIOR FILING DATE: 1995-04-21
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent in version 3.1
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Best Local Similarity 54.1%  Pred. No. 3.9e-48;
Matches 470;  Conservative 0;  Mismatches 386;  Indels 12;  Gaps 3;

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Qy      121  GGTATGATTTAGTTATCTCATCGATACGG---AAGAGACAAACTCAATCAGACCCG 177
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Qy      178  TATACGCAACAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAAAG 237
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Qy      292  GTGGCAAGCGCGCTTGGATTTTGAAGATCGCGTTGCCCTTGGTAGCTAAGCGTGGAGCC 351
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Qy      352  TATATGGAAGAAAGCGGCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCA 411
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Qy      472  AACTATAACACACCTGCACAAATCGTCATTGCTGGAGAAAGTGGTGCAGTTGATCAGCG 531
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Qy      532  GTTGAACCTTTGCAAGNAGCGGTGCCAACGCTTGATTCCTCTTAAGGTGTCAGGTCCC 591
Db      171967  GCTGCATTATGTAAGAGAGCAGGGGCGAAACGTGTCATTCGCGTTAGCTGTGACGCTACCT 171908
Qy      592  TTTCACACCGCTCTCTCTTGAGCCTGCTAGCCAGAAAACACTAGCTGAAAACCTTAGCTCAGGT- 650
Db      171907  TCTCACTGTGCAATTAATGAACCTGCGAGCGGCAATTAGCGGTAAACACTTAGAATAAT 171848
Qy      651  --AAGTTTTTCAGATTTTACTTGTCCCTAGTCGGCAATACAGAACTGCTGTGATGCAA 708
Db      171847  CAAATTAATACCAACAATATCGGTATTAAATAACGTTGATGTAAGAGCTGAACTGAACTGAA 171788
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QY 709 AAAGAGGACATTGCTCAGCTCTTGACGGTCAGGTCAGGAACCGTTTCGTTTCTATGAA 768
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 QY 769 AGTATTGGGTCATGCAAGAGCAGGCATAGCAACTTTATCGAGATTGGACCGGGGAAA 828
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 Db 171667 GTATTAAATGGTTTAAACCAACGCATTG 171640

Search completed: June 11, 2003, 19:58:48
 Job time : 707 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 11, 2003, 20:02:58 ; Search time 233 Seconds
(without alignments)
846.731 Million cell updates/sec

Title: US-09-308-397-2

Perfect score: 1518

Sequence: 1 MTTFALFAGGAGYLGWGR.....QTAHLARVEDQASIVALEK 306

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA Main.*

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- 27: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1518	100.0	306	17	US-09-308-397-2
2	1518	100.0	306	19	US-09-583-110-3912
3	1518	100.0	306	21	US-09-752-069A-143
4	1518	100.0	306	27	US-60-174-089-143
5	1518	100.0	307	15	US-09-107-433-3397
6	1515	99.8	306	1	PCT-US97-22578-171

7	1514	99.7	306	1	PCT-US02-03987-13580
8	1514	99.7	306	22	US-09-815-242-13580
9	1514	99.7	306	24	US-10-072-851-13580
10	1048	69.0	308	27	US-60-360-039-18370
11	948	62.5	328	15	US-09-107-532-6973
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13	937	61.7	313	1	PCT-US02-03987-10920
14	937	61.7	313	22	US-09-815-242-10920
15	937	61.7	313	24	US-10-072-851-10920
16	937	61.7	315	15	US-09-134-000-4987
17	853	56.9	182	17	US-09-308-397-6
18	870	44.1	137	12	US-08-832-030-407
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20	669.5	44.1	317	27	US-60-360-039-23122
21	854	43.1	313	27	US-60-360-039-17325
22	648.5	42.7	333	19	US-09-543-681A-7983
23	646	42.6	306	27	US-60-360-039-19174
24	646	42.6	313	23	US-09-902-340-14562
25	643.5	42.4	309	1	PCT-US02-03987-10125
26	643.5	42.4	309	21	US-09-791-537-94623
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30	636	41.9	312	1	PCT-US02-03987-10975
31	636	41.9	312	21	US-09-791-537-28521
32	636	41.9	312	22	US-09-815-242-10975
33	636	41.9	312	24	US-10-072-851-10975
34	632	41.6	318	21	US-09-791-537-6492
35	619	40.6	311	27	US-60-360-039-10002
36	616.5	40.6	309	21	US-09-791-537-44244
37	613	40.4	122	17	US-09-308-397-4
38	611.5	40.3	307	21	US-09-791-537-122057
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ALIGNMENTS

RESULT 1
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; Sequence 2, Application US/09308397
; GENERAL INFORMATION:
; APPLICANT: Gentry, Daniel R.
; APPLICANT: Lonsdale, John T.
; APPLICANT: Payne, David J.
; APPLICANT: Pearson, Stewart C.
; APPLICANT: Van Aller, Glenn
; TITLE OF INVENTION: Novel Fapd
; FILE REFERENCE: P50593
; CURRENT APPLICATION NUMBER: US/09/308,397
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: US 60/031,160
; EARLIER FILING DATE: 1996-11-18
; EARLIER APPLICATION NUMBER: PCT/US97/20992
; EARLIER FILING DATE: 1997-11-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 306
; TYPE: PPT
; ORGANISM: Streptococcus pneumoniae
US-09-308-397-2

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US-09-583-110-3912
; Sequence 3912, Application US/09583110
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 1998-06-30
; PRIOR FILING DATE: 1998-05-12
; PRIOR FILING DATE: 1998-05-12
; PRIOR FILING DATE: 1998-05-12
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 3912
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-3912

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Best Local Similarity 100.0%; Pred. No. 6.7e-139;
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Db 301 VALLEK 306

RESULT 3

US-09-752-069A-143
; Sequence 143, Application US/09752069A
; GENERAL INFORMATION:
; APPLICANT: Dougherty, Thomas J.
; APPLICANT: Pucci, Michael J.
; APPLICANT: Dougherty, Brian A.
; APPLICANT: Davidson, Daniel B.
; APPLICANT: Bruccoleri, Robert E.
; APPLICANT: Thanassi, Jane A.
; APPLICANT: Farmer II, Bennett T.
; TITLE OF INVENTION: NOVEL BACTERIAL GENES AND PROTEINS THAT ARE ESSENTIAL
; FILE REFERENCE: FOR CELL VIABILITY AND THEIR USES
; FILE REFERENCE: P0001NP
; CURRENT APPLICATION NUMBER: US/09/752,069A
; PRIOR FILING DATE: 2000-12-29
; PRIOR FILING DATE: 60/174,089
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 143
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-752-069A-143

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QY 241 AQLLTRQVKEPVRVYESIGVMQEAGISNFIETPGKVLSGFVKKIDQTAHLAHVEDQASL 300
Db 241 AQLLTRQVKEPVRVYESIGVMQEAGISNFIETPGKVLSGFVKKIDQTAHLAHVEDQASL 300
QY 301 VALLEK 306
Db 301 VALLEK 306

RESULT 4

US-60-174-089-143
; Sequence 143, Application US/60174089
; GENERAL INFORMATION:
; APPLICANT: Dougherty, Thomas J.
; APPLICANT: Pucci, Michael J.
; APPLICANT: Dougherty, Brian A.
; APPLICANT: Davidson, Daniel B.
; TITLE OF INVENTION: NOVEL BACTERIAL GENES AND PROTEINS THAT ARE ESSENTIAL
; FILE REFERENCE: FOR CELL VIABILITY AND THEIR USES
; FILE REFERENCE: 30436.44USP1
; CURRENT APPLICATION NUMBER: US/60/174,089
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 226

```

SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOPHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: misc.feature
LOCATION: (B) LOCATION 1...307
SEQUENCE DESCRIPTION: SEQ ID NO: 3397:
US-09-107-433-3397

Query Match 100.0%; Score 1518; DB 15; Length 307;
Best Local Similarity 100.0%; Pred. No. 6.8e-139;
Matches 306; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 MTKTAFIFAGQAGYQLGMRDFDQVPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY 60
DB 2 MTKTAFIFAGQAGYQLGMRDFDQVPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY 61
QY 61 TPAIATSVAIYRLIQEKGYQPDWVAGLSLGEYSALVAGSALDFEDAVLVAKRQAYME 120
DB 62 TPAIATSVAIYRLIQEKGYQPDWVAGLSLGEYSALVAGSALDFEDAVLVAKRQAYME 121
QY 121 EAPADSGKMWAVLNPVEVIEEACOKASELGVTVPANNYNTPAQIVIAGEWVADVRAVEL 180
DB 122 EAPADSGKMWAVLNPVEVIEEACOKASELGVTVPANNYNTPAQIVIAGEWVADVRAVEL 181
QY 181 LQAGAKRLIPLKVSQPFHTTALPEASQKLAETLAQVSESDFTCLPLVGNTEAAVMQKEDI 240
DB 182 LQAGAKRLIPLKVSQPFHTTALPEASQKLAETLAQVSESDFTCLPLVGNTEAAVMQKEDI 241
QY 241 AQLLTQVKEPVPFYESIGVMQAGISNFIETGPGKVLGSGFVKKIDQTAHLAHVEQASL 300
DB 242 AQLLTQVKEPVPFYESIGVMQAGISNFIETGPGKVLGSGFVKKIDQTAHLAHVEQASL 301
QY 301 VALLEK 306
DB 302 VALLEK 307

RESULT 6
PCT-US97-22578-171
; Sequence 171, Application PC/TUS9722578
; GENERAL INFORMATION:
; APPLICANT: Baitz, Richard H.
; APPLICANT: Burgett, Stanley G.
; APPLICANT: Dehoff, Bradley S.
; APPLICANT: Jaskunas Jr., Stanley R.
; APPLICANT: Mills, Bradley J.
; APPLICANT: Norris, Franklin H.
; APPLICANT: Peery, Robert B.
; APPLICANT: Rostek Jr., Paul R.
; APPLICANT: Skatrud, Paul L.
; APPLICANT: Smith, Michele C.
; APPLICANT: Rockey, Pamela K.
; APPLICANT: Young-Bellido, Michele
; TITLE OF INVENTION: Streptococcus pneumoniae DNA Sequences
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: U.S.
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0. Version #1.30

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/22578
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Webster, Thomas D.
; REGISTRATION NUMBER: 39,872
; REFERENCE/DOCKET NUMBER: X-11162
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-3334
; INFORMATION FOR SEQ ID NO: 171:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 306 amino acids
; TYPE: amino acid
; STRANDEDNESS: Not Relevant
; TOPOLOGY: Not Relevant
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PCT-US97-22578-171

Query Match          99.7%; Score 1514; DB 1; Length 306;
Best Local Similarity 99.7%; Pred. No. 1.7e-138;
Matches 305; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTKTAFAGGGAQYLGMRDFYDQYPIVKETIDRASQVLYGLDRLYLIDTEEDKLNQTRY 60
DB 1 MTKTAFAGGGAQYLGMRDFYDQYPIVKETIDRASQVLYGLDRLYLIDTEEDKLNQTRY 60

QY 61 TOPAILATSAIYRLLOEKGYQDMVAGLSLGEYSALVSGALDFEDAVALKRGAYME 120
DB 61 TOPAILATSAIYRLLOEKGYQDMVAGLSLGEYSALVSGALDFEDAVALKRGAYME 120

QY 121 EAPADSGKMWAVLNPVEIEACQKASELGWVTPANNYTPAQIVIAGEVAVDRAVEL 180
DB 121 EAPADSGKMWAVLNPVEIEACQKASELGWVTPANNYTPAQIVIAGEVAVDRAVEL 180

QY 181 LQAGAKRLIPLKVSQPFHTALLEPASQKLAETLAQVSFSDFTCPVLVGNTEAAVMQKEDI 240
DB 181 LQAGAKRLIPLKVSQPFHTALLEPASQKLAETLAQVSFSDFTCPVLVGNTEAAVMQKEDI 240

QY 241 AQLLTQVKEPVRFYESIGVMQEAGISNFIETGPGKVLGSGFVKKIDQTAHLAHVEDQASL 300
DB 241 AQLLTQVKEPVRFYESIGVMQEAGISNFIETGPGKVLGSGFVKKIDQTAHLAHVEDQASL 300

QY 301 VALLEK 306
DB 301 VALLEK 306

RESULT 7
PCI-US02-03987-13580
; Sequence 13580, Application PC/TUS0203987
; GENERAL INFORMATION:
; APPLICANT: Elittra Pharmaceuticals, Inc.
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C
; TITLE OF INVENTION: Proliferation
; FILE REFERENCE: ELITRA.028VPC
; CURRENT APPLICATION NUMBER: PCT/US02/03987
; CURRENT FILING DATE: 2002-02-02
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13580
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; PCT-US02-03987-13580

Query Match          99.7%; Score 1514; DB 1; Length 306;
Best Local Similarity 99.7%; Pred. No. 1.7e-138;
Matches 305; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTKTAFAGGGAQYLGMRDFYDQYPIVKETIDRASQVLYGLDRLYLIDTEEDKLNQTRY 60
DB 1 MTKTAFAGGGAQYLGMRDFYDQYPIVKETIDRASQVLYGLDRLYLIDTEEDKLNQTRY 60

QY 61 TOPAILATSAIYRLLOEKGYQDMVAGLSLGEYSALVSGALDFEDAVALKRGAYME 120
DB 61 TOPAILATSAIYRLLOEKGYQDMVAGLSLGEYSALVSGALDFEDAVALKRGAYME 120

QY 121 EAPADSGKMWAVLNPVEIEACQKASELGWVTPANNYTPAQIVIAGEVAVDRAVEL 180
DB 121 EAPADSGKMWAVLNPVEIEACQKASELGWVTPANNYTPAQIVIAGEVAVDRAVEL 180

QY 181 LQAGAKRLIPLKVSQPFHTALLEPASQKLAETLAQVSFSDFTCPVLVGNTEAAVMQKEDI 240
DB 181 LQAGAKRLIPLKVSQPFHTALLEPASQKLAETLAQVSFSDFTCPVLVGNTEAAVMQKEDI 240

QY 241 AQLLTQVKEPVRFYESIGVMQEAGISNFIETGPGKVLGSGFVKKIDQTAHLAHVEDQASL 300
DB 241 AQLLTQVKEPVRFYESIGVMQEAGISNFIETGPGKVLGSGFVKKIDQTAHLAHVEDQASL 300

QY 301 VALLEK 306
DB 301 VALLEK 306

RESULT 8
US-09-815-242-13580
; Sequence 13580, Application US/09815242
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13580
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; US-09-815-242-13580

Query Match          99.7%; Score 1514; DB 22; Length 306;
Best Local Similarity 99.7%; Pred. No. 1.7e-138;
Matches 305; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTKTAFAGGGAQYLGMRDFYDQYPIVKETIDRASQVLYGLDRLYLIDTEEDKLNQTRY 60
DB 1 MTKTAFAGGGAQYLGMRDFYDQYPIVKETIDRASQVLYGLDRLYLIDTEEDKLNQTRY 60
```

QY 61 TOPAILATSVAILRLQKGYQPDWVAGLSLGEYSALVAGSALDGEDAVALVAKRGAYME 120
DB 61 TOPAILATSVAILRLQKGYQPDWVAGLSLGEYSALVAGSALDGEDAVALVAKRGAYME 120
QY 121 EAPADSGKMWAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVAVDRAVEL 180
DB 121 EAPADSGKMWAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVAVDRAVEL 180
QY 181 LOEAGAKELIPLKVGSGPHTALLBPASOKLAETIAQVSFSDFTCLVGNTEAAVMQKEDI 240
DB 181 LOEAGAKELIPLKVGSGPHTALLBPASOKLAETIAQVSFSDFTCLVGNTEAAVMQKEDI 240
QY 241 AQLLTQVKEPVRVYESIGVMOEAGISNFIETIGPKVLSGFVKKIDQTAHLAHVEDQASL 300
DB 241 AQLLTQVKEPVRVYESIGVMOEAGISNFIETIGPKVLSGFVKKIDQTAHLAHVEDQASL 300
QY 301 VALLEK 306
DB 301 VALLEK 306

RESULT 9

US-10-072-851-13580

; Sequence 13580, Application US/10072851

; GENERAL INFORMATION:

; APPLICANT: Carr, Grant J.

; APPLICANT: Xu, H. Howard

; APPLICANT: Foulkes, J. Gordon

; APPLICANT: Zamudio, Carlos

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Karl L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John D.

; APPLICANT: Yamamoto, Robert T.

; APPLICANT: Roemer, Terry

; APPLICANT: Jiang, Bo

; APPLICANT: Boone, Charles

; APPLICANT: Bussey, Howard

; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits

; FILE REFERENCE: ELITRA.028A

; CURRENT APPLICATION NUMBER: US/10/072,851

; PRIOR FILING DATE: 2002-02-08

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; NUMBER OF SEQ ID NOS: 15811

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13580

; LENGTH: 306

; TYPE: PRT

; ORGANISM: Streptococcus pneumoniae

US-10-072-851-13580

Query Match 99.7%; Score 1514; DB 24; Length 306;

Best Local Similarity 99.7%; Pred. No. 1.7e-138;

Matches 305; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTKTAFAGGGAQVGLMGGRFYDQYPIVKETIDRASQVGLDYRLYIDTEEDKLNQTRY 60
DB 1 MTKTAFAGGGAQVGLMGGRFYDQYPIVKETIDRASQVGLDYRLYIDTEEDKLNQTRY 60

QY 61 TOPAILATSVAILRLQKGYQPDWVAGLSLGEYSALVAGSALDGEDAVALVAKRGAYME 120
DB 61 TOPAILATSVAILRLQKGYQPDWVAGLSLGEYSALVAGSALDGEDAVALVAKRGAYME 120

QY 121 EAPADSGKMWAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVAVDRAVEL 180
DB 121 EAPADSGKMWAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVAVDRAVEL 180

QY 181 LOEAGAKELIPLKVGSGPHTALLBPASOKLAETIAQVSFSDFTCLVGNTEAAVMQKEDI 240
DB 181 LOEAGAKELIPLKVGSGPHTALLBPASOKLAETIAQVSFSDFTCLVGNTEAAVMQKEDI 240

QY 241 AQLLTQVKEPVRVYESIGVMOEAGISNFIETIGPKVLSGFVKKIDQTAHLAHVEDQASL 300
DB 241 AQLLTQVKEPVRVYESIGVMOEAGISNFIETIGPKVLSGFVKKIDQTAHLAHVEDQASL 300
QY 301 VALLEK 306
DB 301 VALLEK 306

RESULT 10

US-60-360-039-18370

; Sequence 18370, Application US/60360039

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Chen, Xianfeng

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)A

; CURRENT APPLICATION NUMBER: US/60/360,039

; CURRENT FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 18370

; LENGTH: 308

; TYPE: PRT

; ORGANISM: Lactococcus lactis

US-60-360-039-18370

Query Match 69.0%; Score 1048; DB 27; Length 308;

Best Local Similarity 67.5%; Pred. No. 5.1e-93;

Matches 208; Conservative 40; Mismatches 58; Indels 2; Gaps 1;

QY 1 MTKTAFAGGGAQVGLMGGRFYDQYPIVKETIDRASQVGLDYRLYIDTEEDKLNQTRY 60
DB 1 MTKTAFAGGGAQVGLMGGRFYDQYPIVKETIDRASQVGLDYRLYIDTEEDKLNQTRY 60

QY 61 TOPAILATSVAILRLQKGYQPDWVAGLSLGEYSALVAGSALDGEDAVALVAKRGAYME 120
DB 61 TOPAILATSVAILRLQKGYQPDWVAGLSLGEYSALVAGSALDGEDAVALVAKRGAYME 120

QY 121 EAPADSGKMWAVLNTPVEVIEEACQKASEL--GVVTPANYNTPAQIVIAGEVAVDRAV 178
DB 121 EAPADSGKMWAVLNTPVEVIEEACQKASEL--GVVTPANYNTPAQIVIAGEVAVDRAV 180

QY 179 ELLOEAGAKELIPLKVGSGPHTALLBPASOKLAETIAQVSFSDFTCLVGNTEAAVMQKE 238
DB 181 ELLOEAGAKELIPLKVGSGPHTALLBPASOKLAETIAQVSFSDFTCLVGNTEAAVMQKE 240

QY 239 DIAQLLTQVKEPVRVYESIGVMOEAGISNFIETIGPKVLSGFVKKIDQTAHLAHVEDQASL 298
DB 241 EVKGLLTQVMEPVRVYESVETMQKLGATRFTEVGGPRLSGFIKKIDKNAEIANVENLA 300

QY 299 SLVALLEK 306

DB 301 SPEALINQ 308

RESULT 11

US-09-107-532-6973

; Sequence 6973, Application US/09107532

; GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

; TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR

; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

; NUMBER OF SEQUENCES: 7308

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENOME THERAPEUTICS CORPORATION

; STREET: 100 Beaver Street

; CITY: Waltham


```

; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER:
; OPERATING SYSTEM:
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532
; FILING DATE:
; APPLICATION NUMBER: 60/085598
; FILING DATE: May 14, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6973:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1...328
; US-09-107-532-6973

Query Match 62.5%; Score 946; DB 15; Length 328;
Best Local Similarity 61.6%; Pred. No. 3.2e-83;
Matches 188; Conservative 50; Mismatches 63; Indels 4; Gaps 2;

Qy 3 KTAFLPAGQAQYLGMRDFDYQYPTVKETIDRASQVLYGLDYLYLDTDEEDKLNQTRYTQ 62
Db 25 KTAFLPFGGQAQYQGMKDLYE-AYVKQTFDEASEILGYDMAELCFTENELDQTYTQ 83
Qy 63 PAIATSVAIYRLLOEKGYQPDVAGLSLGEYSALVASCALDFEDAVALKVAKGAYMTEA 122
Db 84 PAITVSIAYYRLKXHGHIIPDAALGLSLGEYSALVASCALDFEDAVALKVAKGAYMTEA 143
Qy 123 APADSGMVAVLTPTVEVIEEACQKASELGVTPPANYPNTPAQIVIAGEVAVDRAVELLQ 182
Db 144 TPAGSGMVAVMNAPITETIEESCHEASKYGIYSPANYNTPQQIVIGGEEKAVDEAVLLIK 203
Qy 183 EAGAKRLIPLKVSPPHTALPEASOKLAETLAQVSFSDFTCPVLGNTTEAAVMQKEDIAQ 242
Db 204 EKGFKMIPLVNSGPPHTALEPAKKLAKDLSQTFSEPSPIISNTTTEIMKKETIAG 263
Qy 243 LLTRQVKEPVRFYESIGVMQEGAGISNFIIGPKVLSGFVKKIDQTAHLAHVEDQASL-- 300
Db 264 LLEQQVMQPVRFYESIHLKLTIGIEQVIEVGPGLSGVLSGFMKKIDKTIPLVRVENKQTFDE 323
Qy 301 -VALL 304
Db 324 TIAIL 328

RESULT 12
US-09-107-532A-6973
; Sequence 6973: Application US/09107532A
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

```

```

; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6973:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...328
; SEQUENCE DESCRIPTION: SEQ ID NO: 6973:
US-09-107-532A-6973

Query Match 62.5%; Score 946; DB 15; Length 328;
Best Local Similarity 61.6%; Pred. No. 3.2e-83;
Matches 188; Conservative 50; Mismatches 63; Indels 4; Gaps 2;

Qy 3 KTAFLPAGQAQYLGMRDFDYQYPTVKETIDRASQVLYGLDYLYLDTDEEDKLNQTRYTQ 62
Db 25 KTAFLPFGGQAQYQGMKDLYE-AYVKQTFDEASEILGYDMAELCFTENELDQTYTQ 83
Qy 63 PAIATSVAIYRLLOEKGYQPDVAGLSLGEYSALVASCALDFEDAVALKVAKGAYMTEA 122
Db 84 PAITVSIAYYRLKXHGHIIPDAALGLSLGEYSALVASCALDFEDAVALKVAKGAYMTEA 143
Qy 123 APADSGMVAVLTPTVEVIEEACQKASELGVTPPANYPNTPAQIVIAGEVAVDRAVELLQ 182
Db 144 TPAGSGMVAVMNAPITETIEESCHEASKYGIYSPANYNTPQQIVIGGEEKAVDEAVLLIK 203
Qy 183 EAGAKRLIPLKVSPPHTALPEASOKLAETLAQVSFSDFTCPVLGNTTEAAVMQKEDIAQ 242
Db 204 EKGFKMIPLVNSGPPHTALEPAKKLAKDLSQTFSEPSPIISNTTTEIMKKETIAG 263
Qy 243 LLTRQVKEPVRFYESIGVMQEGAGISNFIIGPKVLSGFVKKIDQTAHLAHVEDQASL-- 300
Db 264 LLEQQVMQPVRFYESIHLKLTIGIEQVIEVGPGLSGVLSGFMKKIDKTIPLVRVENKQTFDE 323
Qy 301 -VALL 304
Db 324 TIAIL 328

```

```
RESULT 13
PCT-US02-03987-10920
; Sequence 10920, Application PC/TUS0203987
; GENERAL INFORMATION:
; APPLICANT: Elitria Pharmaceuticals, Inc.
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C
; FILE REFERENCE: ELITRA.028VPC
; CURRENT APPLICATION NUMBER: PCT/US02/03987
; CURRENT FILING DATE: 2002-02-02
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10920
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
PCT-US02-03987-10920

Query Match      61.7%; Score 937; DB 1; Length 313;
Best Local Similarity 61.9%; Pred. No. 3.5e-82;
Matches 187; Conservative 40; Mismatches 75; Indels 0; Gaps 0;

QY 3 KTAFLPAGGQAQYLGMRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRYTQ 62
Db 6 KTAFLPAGGQAQYQGMGEELYHQEAIVRETFDEASHILGYEMAEELCTENERLNETEY 65
QY 63 PAIATSVAIYRLLOBKGYQPDVAGLSLGEYSALVSGALDPEDAVLVAKRGAYMEEA 122
Db 66 PAIATSVAFYRLLOKGLTFDVAAGLSLGEYSALVSGALRFSFAVALVQKRGQYMTA 125
QY 123 APADSGKQWAVLNTPEVEIEACQKASELGVVTPANTYNTPAQIVIAGEVVAVDRAVELLQ 182
Db 126 APOGTGKQWAVMNAEREVIEKACQEAFAFIVAPANTYNTPOQIVIGGEVAAVDQANTLLK 185
QY 183 BAGAKRLIPLKVSQPFHTALLPASPQKLAETLAQVSDFTCPVLGNTAAVWQKEDIAQ 242
Db 186 EAGVKRMIPLNVSGPFHTALLQSPASKKLAQDLAKNFQWQIPVINSNTTAEIMPQEA 245
QY 243 LLTRQVKPEVRFYESIGVMOEAGISNFIETGPGKVLGSGFKKIDQTAHLAHVEDQASLVA 302
Db 246 LLEKQVMSAVRFDSEIETMKANVGTMIIEVGPCKTLTGFKVKIDKTIEMHRVEDVATLTE 305
QY 303 LL 304
Db 306 TL 307

RESULT 14
US-09-815-242-10920
; Sequence 10920, Application US/09815242
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
```

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; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10920
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10920

Query Match      61.7%; Score 937; DB 22; Length 313;
Best Local Similarity 61.9%; Pred. No. 3.5e-82;
Matches 187; Conservative 40; Mismatches 75; Indels 0; Gaps 0;

QY 3 KTAFLPAGGQAQYLGMRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRYTQ 62
Db 6 KTAFLPAGGQAQYQGMGEELYHQEAIVRETFDEASHILGYEMAEELCTENERLNETEY 65
QY 63 PAIATSVAIYRLLOBKGYQPDVAGLSLGEYSALVSGALDPEDAVLVAKRGAYMEEA 122
Db 66 PAIATSVAFYRLLOKGLTFDVAAGLSLGEYSALVSGALRFSFAVALVQKRGQYMTA 125
QY 123 APADSGKQWAVLNTPEVEIEACQKASELGVVTPANTYNTPAQIVIAGEVVAVDRAVELLQ 182
Db 126 APOGTGKQWAVMNAEREVIEKACQEAFAFIVAPANTYNTPOQIVIGGEVAAVDQANTLLK 185
QY 183 BAGAKRLIPLKVSQPFHTALLPASPQKLAETLAQVSDFTCPVLGNTAAVWQKEDIAQ 242
Db 186 EAGVKRMIPLNVSGPFHTALLQSPASKKLAQDLAKNFQWQIPVINSNTTAEIMPQEA 245
QY 243 LLTRQVKPEVRFYESIGVMOEAGISNFIETGPGKVLGSGFKKIDQTAHLAHVEDQASLVA 302
Db 246 LLEKQVMSAVRFDSEIETMKANVGTMIIEVGPCKTLTGFKVKIDKTIEMHRVEDVATLTE 305
QY 303 LL 304
Db 306 TL 307

RESULT 15
US-10-072-851-10920
; Sequence 10920, Application US/10072851
; GENERAL INFORMATION:
; APPLICANT: Carr, Grant J.
; APPLICANT: Xu, H. Howard
; APPLICANT: Foulkes, J. Gordon
; APPLICANT: Zamudio, Carlos
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boote, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C
; FILE REFERENCE: ELITRA.028A
; CURRENT APPLICATION NUMBER: US/10/072,851
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10920
; LENGTH: 313
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; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-10-072-851-10920

Query Match      61.7%; Score 937; DB 24; Length 313;
Best Local Similarity 61.9%; Pred. No. 3.5e-82;
Matches 187; Conservative 40; Mismatches 75; Indels 0; Gaps 0;

QY 3 KTAFLFAQGGAQYLGMRDFYDQYFIVKXETIDRASQVLGYDLRYLIDTBEEDKLNQTRYTQ 62
Db 6 KTAFLFSGGGAQYQGMBELVHQEAIVRFTTDEASHILGYEMAEELCTENERLNETETQ 65
QY 63 PAILATSAIVRLIQEKGVPQDMVAGLSLGEYSALVSGALDFEDAVALVAKRGAYMEEA 122
Db 66 PAILTUSVAFYRLLOQKGLTPDVVAGLSLGEYSALVSGALRFSEAVALVOKRGQYMTFA 125
QY 123 APADSGKMVAVLNTFVEVIEEACQKASBELGVVTPANYNTPAQIVIAGEVVAVDRAVELLQ 182
Db 126 APQGTGKMVAVMNAEREVIERACQASAFGIVAPANYNTPOQIVIGGEVAAVDQAMTLK 185
QY 183 EAGAKELIPLKVSQPFHTALLEPASQKLAETLAQVSPDFTCPVLGVNTEAAVWQKEDIAQ 242
Db 186 EAGVKRMIPLVNSGPFHTALLOPASKKLAQDLAKLNFQTMQIPVISNTTAEINPQEAIOA 245
QY 243 LLTRQVKEPVRFEYBSIGVWQEAGISNFIIEIGPGKVLSCGFVKKIDQTAHLAHVEDQASLVA 302
Db 246 LLEKQVMSAVRPFDSIETMKAMNVGMTIEVGGPKLTGTGVKKIDKTIEMHRVEDVATITE 305
QY 303 LL 304
Db 306 TL 307
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Search completed: June 11, 2003, 20:10:43
Job time : 236 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 11, 2003, 20:03:47 ; Search time 80 Seconds
(without alignments)
867.756 Million cell updates/sec

Title: US-09-308-397-2

Perfect score: 1518

Sequence: 1 MTKTAPLFGAGQYLQMGRL.....QTAHLAHEVDQASLVALLEK 306

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1050967 seqs, 226864292 residues

Total number of hits satisfying chosen parameters: 1050967

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents AA New:*

1: /cgm2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
2: /cgm2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
3: /cgm2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
4: /cgm2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
5: /cgm2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
6: /cgm2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
7: /cgm2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1515	99.8	306	6	US-10-282-122A-73805
2	1108	73.0	306	6	US-10-282-122A-72188
3	1048	69.0	308	6	US-10-369-493-18370
4	1036	68.2	312	6	US-10-282-122A-74709
5	952	62.7	305	6	US-10-282-122A-57575
6	948	62.5	328	6	US-10-417-884-6973
7	937	61.7	309	6	US-10-282-122A-56896
8	937	61.7	315	5	US-09-134-000C-4987
9	937	61.7	315	5	US-09-134-000C-4987
10	937	61.7	315	6	US-10-434-665-4987
11	713.5	47.0	308	6	US-10-282-122A-52133
12	669.5	44.1	317	6	US-10-369-493-23122
13	657.5	43.3	312	6	US-10-282-122A-77375
14	654	43.1	313	6	US-10-369-493-17325
15	649.5	42.8	310	6	US-10-282-122A-68370
16	647	42.6	318	6	US-10-282-122A-52405
17	646	42.6	305	6	US-10-369-493-19174
18	643.5	42.4	309	6	US-10-282-122A-56519
19	643.5	42.4	309	6	US-10-369-493-793
20	636	41.9	312	6	US-10-282-122A-58091
21	628.5	41.4	309	6	US-10-282-122A-78414
22	626	41.2	312	6	US-10-282-122A-67441
23	625.5	41.2	308	6	US-10-282-122A-59351
24	619	40.8	311	6	US-10-369-493-10002
25	616.5	40.6	309	6	US-10-282-122A-75151
26	612.5	40.3	309	6	US-10-282-122A-75888

US-10-282-122A-73805
; Sequence 73805, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73805
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-282-122A-73805

ALIGNMENTS

RESULT 1

US-10-282-122A-73805
; Sequence 73805, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73805
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-282-122A-73805

Query Match 99.8%; Score 1515; DB 6; Length 306;
 Best Local Similarity 99.7%; Pred. No. 4.8e-124;
 Matches 305; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

US-10-282-122A-72188

Query Match 73.0%; Score 1108; DB 6; Length 306;
 Best Local Similarity 71.8%; Pred. No. 1.7e-98;
 Matches 219; Conservative 37; Mismatches 49; Indels 0; Gaps 0;

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 DB 1 MTKTAFAGGQAQYLGMRDFDYDQYPIVKETIDRASQVGLYDLRLIDTEEDKLNQTRY 60

QY 61 TOPAILATSVAIYRLLOEKGYQDMVAGLSLGEYSALVAGSALDGFEDAVALKRGAYME 120
 DB 61 TOPAILATSVAIYRLLOEKGYQDMVAGLSLGEYSALVAGSALDGFEDAVALKRGAYME 120

QY 121 EAPADSGKMWAVLNTPEVEIEACOKASELGWVTPANTYNTPAQIVIAGEVAVDRAVEL 180
 DB 121 EAPADSGKMWAVLNTPEVEIEACOKASELGWVTPANTYNTPAQIVIAGEVAVDRAVEL 180

QY 181 LOEAGAKRLIPLKVSQPFHTALLPASOKLAETLAQVSDFTCPVLGNTEAAVMOKEDI 240
 DB 181 LOEAGAKRLIPLKVSQPFHTALLPASOKLAETLAQVSDFTCPVLGNTEAAVMOKEDI 240

QY 241 AQLLTQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHDQASL 300
 DB 241 AQLLTQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHDQASL 300

QY 301 VALLEK 306
 DB 301 VALLEK 306

RESULT 2

US-10-282-122A-72188

Sequence 72188, Application US/10282122A

GENERAL INFORMATION:

APPLICANT: Wang, Liangau

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari

APPLICANT: Zyskind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

PRIOR FILING DATE: 2003-02-20

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 72188

QY 1 MTKTAFAGGQAQYLGMRDFDYDQYPIVKETIDRASQVGLYDLRLIDTEEDKLNQTRY 60
 DB 1 MTKTAFAGGQAQYLGMRDFDYDQYPIVKETIDRASQVGLYDLRLIDTEEDKLNQTRY 60

QY 61 TOPAILATSVAIYRLLOEKGYQDMVAGLSLGEYSALVAGSALDGFEDAVALKRGAYME 120
 DB 61 TOPAILATSVAIYRLLOEKGYQDMVAGLSLGEYSALVAGSALDGFEDAVALKRGAYME 120

QY 121 EAPADSGKMWAVLNTPEVEIEACOKASELGWVTPANTYNTPAQIVIAGEVAVDRAVEL 180
 DB 121 EAPADSGKMWAVLNTPEVEIEACOKASELGWVTPANTYNTPAQIVIAGEVAVDRAVEL 180

QY 181 LOEAGAKRLIPLKVSQPFHTALLPASOKLAETLAQVSDFTCPVLGNTEAAVMOKEDI 240
 DB 181 LOEAGAKRLIPLKVSQPFHTALLPASOKLAETLAQVSDFTCPVLGNTEAAVMOKEDI 240

QY 241 AQLLTQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHDQASL 300
 DB 241 AQLLTQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHDQASL 300

QY 301 VALLE 305
 DB 301 QAFLD 305

RESULT 3

US-10-369-493-18370

Sequence 18370, Application US/10369493

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 18370

LENGTH: 308

TYPE: PRT

ORGANISM: Lactococcus lactis

US-10-369-493-18370

Query Match 69.0%; Score 1048; DB 6; Length 308;
 Best Local Similarity 67.5%; Pred. No. 3e-83;
 Matches 208; Conservative 40; Mismatches 58; Indels 2; Gaps 1;

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 DB 1 MTKTAFAGGQAQYLGMRDFDYDQYPIVKETIDRASQVGLYDLRLIDTEEDKLNQTRY 60

QY 61 TOPAILATSVAIYRLLOEKGYQDMVAGLSLGEYSALVAGSALDGFEDAVALKRGAYME 120
 DB 61 TOPAILATSVAIYRLLOEKGYQDMVAGLSLGEYSALVAGSALDGFEDAVALKRGAYME 120

QY 121 EAPADSGKMWAVLNTPEVEIEACOKASEL--GVVTPANTYNTPAQIVIAGEVAVDRAV 178
 DB 121 EAPADSGKMWAVLNTPEVEIEACOKASEL--GVVTPANTYNTPAQIVIAGEVAVDRAV 180

QY 179 ELLOEAGAKRLIPLKVSQFFHTALLEPASOKLATLTAQVSFSDFTCPDVONTAAVMQKE 238
DB 181 ELLKEAGVRKLIETLVKSQFFHTALTLPASEKLALELDKIDFRPPELPLIGNTSAKMEND 240
QY 239 DIAQLLTQVKEPVPFYFESIGVMQEAGISNIEIPGKVLSGFVKKIDOTAHLAHVEDQA 298
DB 241 EVKGLLTQVMEPVPFYFESVETMQKLGATRIEIVGPGSVLSGFIKKIDKNAEIANVENIA 300
QY 299 SLVALLEK 306
DB 301 SPEALING 308

RESULT 4
US-10-282-122A-74709
Sequence 74709, Application US/10282122A
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Cart, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282.122A
CURRENT FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-03-21
PRIORITY APPLICATION NUMBER: 60/206,848
PRIORITY FILING DATE: 2000-05-23
PRIORITY APPLICATION NUMBER: 60/207,727
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/230,335
PRIORITY FILING DATE: 2000-09-06
PRIORITY APPLICATION NUMBER: 60/230,347
PRIORITY FILING DATE: 2000-09-09
PRIORITY APPLICATION NUMBER: 60/242,578
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-27
PRIORITY APPLICATION NUMBER: 60/257,931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/267,636
PRIORITY FILING DATE: 2001-02-09
PRIORITY APPLICATION NUMBER: 60/269,308
PRIORITY FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 74709
LENGTH: 312
TYPE: PRT
ORGANISM: Streptococcus pyogenes
US-10-282-122A-74709

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Db 121 EAAPGSGKGVAVVMTDVQVTEIEVCQAAGKGVVAPANTPTESQIVIGQTDVAVNVAVEL 180
QY 181 LOEAGAKELIPLKVGSGPHHTALLESASOKLAETLAQVSPSSDFTCPILVGNTEAAVMQKEDI 240
Db 181 LKERGVKKLIPLNVSGGPHHTALLESASRLJAKELERNFSDFKIPILVGNTEANIMEKDI 240
QY 241 AQLLTQYKQEVRFYSEIGVMQEAAGISNFIETGKVLGSGVKKIDQTAHLAHVEDQASL 300
Db 241 PELLARQVMQEVRFYSDVATIVESGITOQFIEVGPGLVTOGFVKKIDKNLLCTSVENMVSL 300
QY 301 VALLEK 306
Db 301 RLFLDR 306

RESULT 5
US-10-282-122A-57675
; Sequence 57675, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Hasselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57675
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-10-282-122A-57675

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Db 2 KTAFLFSGGAGYQGMKDLVEE-AVVKQTDFEASEILGYDMAELCFTENRDLQOTYTQ 60

QY 63 FAILATSAIYVRLLOEKGYQPDWVAGLSLGEYSALVAGSALDGFEDAVALKRGMAYMEEA 122

Db 61 PAITVSTAYVRLLEKHEGIIIPDAALGLSLGEYSALVAGSALDGFEDAVALKRGMAYMEEA 120

QY 123 APADSGKAVANTVEVEIEBACQKASBLGVVTPANYNTPAQIVIAGEVAVDRAVELLO 182

Db 121 APAGSGKAVANNAPETIEESCHESKYGIVSPANYNTPOQIVIGGEEKAVDRAVELLO 180

QY 183 EAGAKRLIPLKVGSPFHTALLEPASQKLAETIAQVSDFTCPVLVGNTEAAVMQKEDIAG 242

Db 181 EKGFKRMIPLNVSGPFHTALLEPASQKLAETIAQVSDFTCPVLVGNTEAAVMQKEDIAG 240

QY 243 LLTROVKEPVRPYESIGVMQKAGISNFIETIGPKVLSGFVKKIDQTAHLAHVEDQASL-- 300

Db 241 LLEQQVMQVPRFYESIHKLTIGIEVQIEVGGKVLGSGFMKKIDKTIPLVRVENKQTFDE 300

QY 301 -VALL 304

Db 301 TTAIL 305

RESULT 6

US-10-417-884-6973

Sequence 6973, Application US/10417884

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:

ADDRESS: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: PC

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/417,884

FILING DATE: 17-Apr-2003

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Axiniello, Pamela Deneka

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 6973:

SEQUENCE CHARACTERISTICS:

LENGTH: 328 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...328

SEQUENCE DESCRIPTION: SEQ ID NO: 6973:

US-10-417-884-6973

Query Match 62.5%; Score 948; DB 6; Length 328;

Best Local Similarity 61.6%; Pred. No. 1.8e-74;

Matches 188; Conservative 50; Mismatches 63; Indels 4; Gaps 2;

QY 3 KTAFLFAGGAGYQGMKDLVEE-AVVKQTDFEASEILGYDMAELCFTENRDLQOTYTQ 62

Db 25 KTAFLFSGGAGYQGMKDLVEE-AVVKQTDFEASEILGYDMAELCFTENRDLQOTYTQ 83

QY 63 FAILATSAIYVRLLOEKGYQPDWVAGLSLGEYSALVAGSALDGFEDAVALKRGMAYMEEA 122

Db 84 PAITVSTAYVRLLEKHEGIIIPDAALGLSLGEYSALVAGSALDGFEDAVALKRGMAYMEEA 143

QY 123 APADSGKAVANTVEVEIEBACQKASBLGVVTPANYNTPAQIVIAGEVAVDRAVELLO 182

Db 144 TPAGSGKAVANNAPETIEESCHESKYGIVSPANYNTPOQIVIGGEEKAVDRAVELLO 203

QY 183 EAGAKRLIPLKVGSPFHTALLEPASQKLAETIAQVSDFTCPVLVGNTEAAVMQKEDIAG 242

Db 204 EKGFKRMIPLNVSGPFHTALLEPASQKLAETIAQVSDFTCPVLVGNTEAAVMQKEDIAG 263

QY 243 LLTROVKEPVRPYESIGVMQKAGISNFIETIGPKVLSGFVKKIDQTAHLAHVEDQASL-- 300

Db 264 LLEQQVMQVPRFYESIHKLTIGIEVQIEVGGKVLGSGFMKKIDKTIPLVRVENKQTFDE 323

QY 301 -VALL 304

Db 324 TTAIL 328

RESULT 7

US-10-282-122A-56896

Sequence 56896, Application US/10282122A

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari

APPLICANT: Zyskind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56896
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; US-10-282-122A-56896

Query Match      61.7%; Score 937; DB 6; Length 309;
Best Local Similarity 61.9%; Pred. No. 1.5e-73;
Matches 187; Conservative 40; Mismatches 75; Indels 0; Gaps 0;

QY 3 KTAFLFAGGAGQAYLGMGRDQYPIVKEITDRASQVGLGDLRYLIDTDEDKLNQTRYQ 62
DB 2 KTAFLFSGGAGQAYGGMGEELYHQEAIIVRETDFDASHILGYEMAEELCTENERLNTEYQ 61
QY 63 PAIATSVAILRLQEKGYQPDVAGLSLGEYSALVSGALDFEDAVALKRGAYMEEA 122
DB 62 PAITVSVAFYRLQLQKGLTPDVVAGLSLGEYSALVSGALRSEAVLVKRGQYMTA 121
QY 123 APADSGKQWAVLTPVEIEACQKASELGVVTPANTPAQIVIAGEVAVDRAVELLQ 182
DB 122 APOGTGKQWAVMNAEREVIEKACQASAFGIVAPANTPQQIVIGEVAADVQAMTLK 181
QY 183 EAGAKRLIPLKVSPPHTALLEPASOKLAETLAQVSFSDFTCLVGNTEAAVNMCKEDIAQ 242
DB 182 EAGKRMIPLVNSGPFHTALLQPKSKLAQDLAKLNFQMTQIPVISNTTAEIMPQEAIA 241
QY 243 LLTRQVKPEVPFYESIGVMQEGAGISNFIETGPKVLSGFVKKIDQTAHLAHVEDQASLVA 302
DB 242 LLEKQVMSAVRFEDSIETMKAMVGTMTIEVPGKTLTGTFVKKIDKTIEMHVEDVATLTE 301
QY 303 LL 304
DB 302 TL 303

Query Match      61.7%; Score 937; DB 5; Length 315;
Best Local Similarity 61.9%; Pred. No. 1.5e-73;
Matches 187; Conservative 40; Mismatches 75; Indels 0; Gaps 0;

RESULT 8
US-09-134-000C-4987
; Sequence 4987, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4987
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; US-09-134-000C-4987

QY 3 KTAFLFAGGAGQAYLGMGRDQYPIVKEITDRASQVGLGDLRYLIDTDEDKLNQTRYQ 62
DB 8 KTAFLFSGGAGQAYGGMGEELYHQEAIIVRETDFDASHILGYEMAEELCTENERLNTEYQ 67
QY 63 PAIATSVAILRLQEKGYQPDVAGLSLGEYSALVSGALDFEDAVALKRGAYMEEA 122
DB 68 PAITVSVAFYRLQLQKGLTPDVVAGLSLGEYSALVSGALRSEAVLVKRGQYMTA 127
QY 123 APADSGKQWAVLTPVEIEACQKASELGVVTPANTPAQIVIAGEVAVDRAVELLQ 182
DB 128 APOGTGKQWAVMNAEREVIEKACQASAFGIVAPANTPQQIVIGEVAADVQAMTLK 187
QY 183 EAGAKRLIPLKVSPPHTALLEPASOKLAETLAQVSFSDFTCLVGNTEAAVNMCKEDIAQ 242
DB 188 EAGKRMIPLVNSGPFHTALLQPKSKLAQDLAKLNFQMTQIPVISNTTAEIMPQEAIA 247
QY 243 LLTRQVKPEVPFYESIGVMQEGAGISNFIETGPKVLSGFVKKIDQTAHLAHVEDQASLVA 302
DB 248 LLEKQVMSAVRFEDSIETMKAMVGTMTIEVPGKTLTGTFVKKIDKTIEMHVEDVATLTE 307
QY 303 LL 304
DB 308 TL 309
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RESULT 10
US-10-434-665-4987
; Sequence 4987, Application US/10434665
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: PATH03-09
; CURRENT APPLICATION NUMBER: US/10/434,665
; CURRENT FILING DATE: 2003-05-14
; PRIOR FILING DATE: 1998-08-13
```

```
Db 188 EAGKRMIPLVNSGPFHTALLQPKSKLAQDLAKLNFQMTQIPVISNTTAEIMPQEAIA 247
QY 243 LLTRQVKPEVPFYESIGVMQEGAGISNFIETGPKVLSGFVKKIDQTAHLAHVEDQASLVA 302
DB 248 LLEKQVMSAVRFEDSIETMKAMVGTMTIEVPGKTLTGTFVKKIDKTIEMHVEDVATLTE 307
QY 303 LL 304
DB 308 TL 309

RESULT 9
US-09-134-000C-4987
; Sequence 4987, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4987
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; US-09-134-000C-4987

Query Match      61.7%; Score 937; DB 5; Length 315;
Best Local Similarity 61.9%; Pred. No. 1.5e-73;
Matches 187; Conservative 40; Mismatches 75; Indels 0; Gaps 0;

QY 3 KTAFLFAGGAGQAYLGMGRDQYPIVKEITDRASQVGLGDLRYLIDTDEDKLNQTRYQ 62
DB 8 KTAFLFSGGAGQAYGGMGEELYHQEAIIVRETDFDASHILGYEMAEELCTENERLNTEYQ 67
QY 63 PAIATSVAILRLQEKGYQPDVAGLSLGEYSALVSGALDFEDAVALKRGAYMEEA 122
DB 68 PAITVSVAFYRLQLQKGLTPDVVAGLSLGEYSALVSGALRSEAVLVKRGQYMTA 127
QY 123 APADSGKQWAVLTPVEIEACQKASELGVVTPANTPAQIVIAGEVAVDRAVELLQ 182
DB 128 APOGTGKQWAVMNAEREVIEKACQASAFGIVAPANTPQQIVIGEVAADVQAMTLK 187
QY 183 EAGAKRLIPLKVSPPHTALLEPASOKLAETLAQVSFSDFTCLVGNTEAAVNMCKEDIAQ 242
DB 188 EAGKRMIPLVNSGPFHTALLQPKSKLAQDLAKLNFQMTQIPVISNTTAEIMPQEAIA 247
QY 243 LLTRQVKPEVPFYESIGVMQEGAGISNFIETGPKVLSGFVKKIDQTAHLAHVEDQASLVA 302
DB 248 LLEKQVMSAVRFEDSIETMKAMVGTMTIEVPGKTLTGTFVKKIDKTIEMHVEDVATLTE 307
QY 303 LL 304
DB 308 TL 309
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; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4987
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-10-434-663-4987

Query Match          61.7%; Score 937; DB 6; Length 315;
-Best Local Similarity 61.9%; Pred. No. 1.5e-73;
Matches 187; Conservative 40; Mismatches 75; Indels 0; Gaps 0;

QY 3 KTAFLFAGGAGQYLGMRGDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRYTO 62
Db 8 KTAFLFAGGAGQYLGMRGDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRYTO 67

QY 63 PAIATSVAIYRLIQKGYQPMVAGLSLGEYSALVSGALDFEDAVALKVAKGAYMSEA 122
Db 68 PAIATSVAIYRLIQKGYQPMVAGLSLGEYSALVSGALDFEDAVALKVAKGAYMSEA 127

QY 123 APADSGKAVLNTPEVIEEACQKASELGVTPANYPNTPAQIIVAGEVAVDRAVELLO 182
Db 128 APADSGKAVLNTPEVIEEACQKASELGVTPANYPNTPAQIIVAGEVAVDRAVELLO 187

QY 183 EAGAKELIPLKVSPPHTALLESASOKLAETIAQVFSDFCTPLVGNTEAAVMQKEDIAQ 242
Db 188 EAGKEMIPLVNSPHTALLESASOKLAETIAQVFSDFCTPLVGNTEAAVMQKEDIAQ 247

QY 243 LLTROVKEPVRYESIGVQWQAGISNFIIGPKVLSGVFKKIDQTAHLAHVEDQASLVA 302
Db 248 LLEKQVMSAVRFDSEIETKMANVGTMIIEVGPCKTLTGFKKIDKTIEMHRVEDVATLTE 307

QY 303 LL 304
Db 308 TL 309

RESULT 11
US-10-282-122A-52133
; Sequence 52133, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27

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; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 52133
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Clostridium acetobutylicum
US-10-282-122A-52133

Query Match          47.0%; Score 713.5; DB 6; Length 308;
-Best Local Similarity 48.5%; Pred. No. 4.9e-54;
Matches 147; Conservative 56; Mismatches 97; Indels 3; Gaps 3;

QY 1 MTKTAFLFAGGAGQYLGMRGDFYDQYPIVKETIDRASQVLGYDLRYL-IDTEEDKLNQTR 59
Db 1 MGKIAFVFSGGQYVGMGKDLVDNYQSAKETFDKADVLGPKISELCPEGKDEELNLT 60

QY 60 YTPAIIATSVAIYRLI-QEKGYPDMVAGLSLGEYSALVSGALDFEDAVALKVAKGAY 118
Db 61 NTPAVALITISIALRALLEEKGIRKPDVAGLSLGEYSAHVCSGFSFEDAVRLVKRGY 120

QY 119 MEAPADSGKAVLNTPEVIEEACQKASELGVTPANYPNTPAQIIVAGEVAVDRAV 178
Db 121 MCEAVPKIGITMAIIGLEGDVVRGICAEQSGEIVEVANNYCPGQIIVAGEVAVESAC 180

QY 179 ELIOEAGAKELIPLKVSPPHTALLESASOKLAETIAQVFSDFCTPLVGN-TEAAVMQK 237
Db 181 TLKESGARITVMSLVSPGPHSTSLKSAEKLBEELKNINIEDMKVPVITNVTGDDVEDK 240

QY 238 EDIAQLLTROVKEPVRYESIGVQWQAGISNFIIGPKVLSGVFKKIDQTAHLAHVEDQ 297
Db 241 DQIKGLLKKQWMSVVRWEDTIRNMDGVDVTFIELGPKTLSSFIKKINKMTIFNIEKA 300

QY 298 ASL 300
Db 301 EDL 303

RESULT 12
US-10-369-493-23122
; Sequence 23122, Application US/10369493
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 23122
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-369-493-23122

Query Match          44.1%; Score 669.5; DB 6; Length 317;
-Best Local Similarity 47.2%; Pred. No. 3.6e-50;
Matches 143; Conservative 47; Mismatches 110; Indels 3; Gaps 3;

QY 1 MTKTAFLFAGGAGQYLGMRGDFYDQYPIVKETIDRASQVLGYDLRYL-IDTEEDKLNQTR 59

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Db 1 MSKIAFLPGGQSQFIMGKELYEQVPAKRLFDDEADETLETKLSSLIFFEGDAEELTLY 60
QY 60 YTOPAILATSAIYRLLOEKGYQPDVAGLSGYSALVAGSALDGFEDAVALVAKRGAYM 119
Db 61 NAQPALLTTSIAVLEKFKESGITPDFTAGHSLGYSALVAGSALDGFEDAVYVTKRGGEFM 120
QY 120 EEAAPADSGKVVAVLNTPEVEIEBACQKASELG-VVTPANVTTPAQIVIAAGEVAVDRAV 178
Db 121 NEAVPAGESGAAIILGMDAEALKQVTDKVTTEGNIVQLANLNCPGQIVISGTAKGVELAS 180
QY 179 ELLQAGAKRLIPLKVSQGFHTALLEPASQKLAETLAQVSFSDFTCLPLVGNTEAAVM-QK 237
Db 181 ELAKENGAKRAIPLEVSQGFHTALLEPASQKLAETLAQVSFSDFTCLPLVGNTEAAVM-QK 240
QY 238 EDIAQLLTQVKEPVRPFYESIGVMOEAGISNFIEIGPGKVLSGFVKKIDOTAHLAHVEDQ 297
Db 241 ADIEKLEQLYSVPRVFESINKLIAEGVTFIEIGPGKVLSGFVKKIDOTAHLAHVEDQ 300
QY 298 ASL 300
Db 301 ETI 303

RESULT 13

US-10-122A-77375
; Sequence 77375, Application US/10282122A
; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Chleen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent version 3.1
; SEQ ID NO: 77375
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-10-122A-77375

Query Match 43.3%; Score 657.5; DB 6; Length 312;

Best Local Similarity 47.4%; Pred. No. 3,9e-49;
Matches 146; Conservative 58; Mismatches 97; Indels 7; Gaps 4;
QY 1 MTKTAPLFAQGAQVLMGRDIFYQYPIVKETIDRASQVLYGVDLYLI-DTDEKLNQTR 59
Db 6 MSKFAIYFPFGQSQAQVLMGRDIFYQYPIVKETIDRASQVLYGVDLYLI-DTDEKLNQTR 65
QY 60 YTOPAILATSAIYRLLOEKGY-QPDVAGLSGYSALVAGSALDGFEDAVALVAKRGAY 118
Db 66 RTQPALLAASVAIRVRWQOLGLEQPAVLAGHSLGYSALVAGSALDGFEDAVALVAKRGAY 125
QY 119 MEEAAPADSGKVVAVLNTPEVEIEBACQKASELG-VVTPANVTTPAQIVIAAGEVAVDRAV 178
Db 126 MQCAVPAGTAMVYIIGLEDEAIAKACADAQGEVVPVFNFSQGVVIAGQKDAVERAG 185
QY 179 ELLQAGAKRLIPLKVSQGFHTALLEPASQKLAETLAQVSFSDFTCLPLVGNTEAAVMQKE 238
Db 186 VLCKGAGAKRLIPLKVSQGFHTALLEPASQKLAETLAQVSFSDFTCLPLVGNTEAAVMQKE 243
QY 239 D---IAQLLTQVKEPVRPFYESIGVMOEAGISNFIEIGPGKVLSGFVKKIDOTAHLAHVE 295
Db 244 DPKIKDALIRQLYSVPRVTECEQMSAGQVKEIEMGFGKVLTLTKRIVTLEGVAVN 303
QY 296 DQASLVAL 303
Db 304 DVASLDVA 311

RESULT 14

US-10-369-493-17325
; Sequence 17325, Application US/10369493
; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO: 17325
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Bacillus halodurans
US-10-369-493-17325

Query Match 43.1%; Score 654; DB 6; Length 313;

Best Local Similarity 45.6%; Pred. No. 8e-49;
Matches 141; Conservative 58; Mismatches 106; Indels 4; Gaps 4;
QY 1 MTKTAPLFAQGAQVLMGRDIFYQYPIVKETIDRASQVLYGVDL-RYLIDTEEDKLNQTR 59
Db 1 MAKVAFLPFGQSQAQVLMGRDIFYQYPIVKETIDRASQVLYGVDL-RYLIDTEEDKLNQTR 59
QY 60 YTOPAILATSAIYRLLOEKGYQPDVAGLSGYSALVAGSALDGFEDAVALVAKRGAYM 119
Db 60 NTQPALLTMTSTAVLSLVREYGIKPDYTAGHSLGYSALVAGSALDGFEDAVYVTKRGGEFM 119
QY 120 EEAAPADSGKVVAVLNTPEVEIEBACQKASELG-VVTPANVTTPAQIVIAAGEVAVDRAV 178
Db 120 EEAAPADSGKVVAVLNTPEVEIEBACQKASELG-VVTPANVTTPAQIVIAAGEVAVDRAV 179
QY 179 ELLQAGAKRLIPLKVSQGFHTALLEPASQKLAETLAQVSFSDFTCLPLVGNTEAAVMQK- 237
Db 180 EEAKEAGAKRVIPLOVSGFHTALLEPASQKLAETLAQVSFSDFTCLPLVGNTEAAVMQK- 239
QY 238 EDIAQLLTQVKEPVRPFYESIGVMOEAGISNFIEIGPGKVLSGFVKKIDOTAHLAHVEDQ 297

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Db 240 ADIRSSLIQVSPVWEDTVRMLBGLVDTFVEIGSGNVLGSLVRKQVRRNVFVSDDR 299
Qy 298 ASLVALLEK 306
   ||: ||:|
Db 300 ASIEAMVKK 308

RESULT 15
US-10-282-122A-68370
; Sequence 68370, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68370
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-10-282-122A-68370

Query Match 42.8%; Score 649.5; DB 6; Length 310;
Best Local Similarity 47.2%; Pred. No. 1.9e-48;
Matches 145; Conservative 51; Mismatches 108; Indels 3; Gaps 3;

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Db 1 MTDFAWVFGQGSQAIGMLAEAEHYPIVTETFAQSDVLYGSLWDLVQNGPSEELNKTW 60
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Qy 119 MEERAPADSGKMWAVLNTVEVEIEECOKASELGVVTPANTPAQIVIAGEVVAVDRAV 178
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Qy 298 ASLVALL 304
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Search completed: June 11, 2003, 20:12:15
Job time : 81 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 11, 2003, 20:17:43 ; Search time 2196 Seconds
(without alignments)
3503.461 Million cell updates/sec

Title: US-09-308-397-2
Perfect score: 1518
Sequence: 1 MTKTAFIFACGQGYLQNGR.....QTAHLARVEDQASLVALLEK 306

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-NO.MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending Patents NA Main:
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Result No.	Score	Query Match	Length	DB ID	Description
1	1518	100.0	921	17	US-09-308-397-1
2	1518	100.0	921	22	US-09-583-110-1251
3	1518	100.0	921	29	US-09-752-069A-30
4	1518	100.0	921	61	US-60-174-089-30
5	1518	100.0	924	15	US-09-107-433-794
6	1518	100.0	19702	41	US-10-158-844-7

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

29: /cgn2_6/ptodata/2/pna/US097B COMB.seq.*	30: /cgn2_6/ptodata/2/pna/US097C COMB.seq.*	31: /cgn2_6/ptodata/2/pna/US098A COMB.seq.*	32: /cgn2_6/ptodata/2/pna/US098B COMB.seq.*	33: /cgn2_6/ptodata/2/pna/US098C COMB.seq.*	34: /cgn2_6/ptodata/2/pna/US099A COMB.seq.*	35: /cgn2_6/ptodata/2/pna/US099B COMB.seq.*	36: /cgn2_6/ptodata/2/pna/US099C COMB.seq.*	37: /cgn2_6/ptodata/2/pna/US099D COMB.seq.*	38: /cgn2_6/ptodata/2/pna/US100A COMB.seq.*	39: /cgn2_6/ptodata/2/pna/US100B COMB.seq.*	40: /cgn2_6/ptodata/2/pna/US101A COMB.seq.*	41: /cgn2_6/ptodata/2/pna/US101B COMB.seq.*	42: /cgn2_6/ptodata/2/pna/US102A COMB.seq.*	43: /cgn2_6/ptodata/2/pna/US102B COMB.seq.*	44: /cgn2_6/ptodata/2/pna/US6001 COMB.seq.*	45: /cgn2_6/ptodata/2/pna/US6002 COMB.seq.*	46: /cgn2_6/ptodata/2/pna/US6003 COMB.seq.*	47: /cgn2_6/ptodata/2/pna/US6004 COMB.seq.*	48: /cgn2_6/ptodata/2/pna/US6005 COMB.seq.*	49: /cgn2_6/ptodata/2/pna/US6006 COMB.seq.*	50: /cgn2_6/ptodata/2/pna/US6007 COMB.seq.*	51: /cgn2_6/ptodata/2/pna/US6008 COMB.seq.*	52: /cgn2_6/ptodata/2/pna/US6009 COMB.seq.*	53: /cgn2_6/ptodata/2/pna/US6010 COMB.seq.*	54: /cgn2_6/ptodata/2/pna/US6011 COMB.seq.*	55: /cgn2_6/ptodata/2/pna/US6012 COMB.seq.*	56: /cgn2_6/ptodata/2/pna/US6013 COMB.seq.*	57: /cgn2_6/ptodata/2/pna/US6014 COMB.seq.*	58: /cgn2_6/ptodata/2/pna/US6015 COMB.seq.*	59: /cgn2_6/ptodata/2/pna/US6016 COMB.seq.*	60: /cgn2_6/ptodata/2/pna/US6017 COMB.seq.*	61: /cgn2_6/ptodata/2/pna/US6018 COMB.seq.*	62: /cgn2_6/ptodata/2/pna/US6019 COMB.seq.*	63: /cgn2_6/ptodata/2/pna/US6020 COMB.seq.*	64: /cgn2_6/ptodata/2/pna/US6021 COMB.seq.*	65: /cgn2_6/ptodata/2/pna/US6022 COMB.seq.*	66: /cgn2_6/ptodata/2/pna/US6023 COMB.seq.*	67: /cgn2_6/ptodata/2/pna/US6024 COMB.seq.*	68: /cgn2_6/ptodata/2/pna/US6025 COMB.seq.*	69: /cgn2_6/ptodata/2/pna/US6026 COMB.seq.*	70: /cgn2_6/ptodata/2/pna/US6027 COMB.seq.*	71: /cgn2_6/ptodata/2/pna/US6028 COMB.seq.*	72: /cgn2_6/ptodata/2/pna/US6029 COMB.seq.*	73: /cgn2_6/ptodata/2/pna/US6030 COMB.seq.*	74: /cgn2_6/ptodata/2/pna/US6031 COMB.seq.*	75: /cgn2_6/ptodata/2/pna/US6032 COMB.seq.*	76: /cgn2_6/ptodata/2/pna/US6033 COMB.seq.*	77: /cgn2_6/ptodata/2/pna/US6034 COMB.seq.*	78: /cgn2_6/ptodata/2/pna/US6035 COMB.seq.*	79: /cgn2_6/ptodata/2/pna/US6036 COMB.seq.*	80: /cgn2_6/ptodata/2/pna/US6037 COMB.seq.*	81: /cgn2_6/ptodata/2/pna/US6038 COMB.seq.*	82: /cgn2_6/ptodata/2/pna/US6039 COMB.seq.*	83: /cgn2_6/ptodata/2/pna/US6040 COMB.seq.*	84: /cgn2_6/ptodata/2/pna/US6041 COMB.seq.*	85: /cgn2_6/ptodata/2/pna/US6042 COMB.seq.*
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8 1515 99.8 945 29 US-09-752-069A-256
9 1515 99.8 3580 1 PCT-US97-22578-43
10 1514 99.7 921 31 PCT-US02-03987-9482
11 1514 99.7 921 31 US-09-815-242-9482
12 1514 99.7 921 39 US-10-072-851-9482
13 1514 99.7 9753 50 US-60-068-175-555
14 1488 98.0 5963 50 US-60-061-998-494
15 1048 69.0 927 80 US-60-360-039-42057
16 952 62.7 2969 49 US-60-050-444-527
17 952 62.7 2969 50 US-60-068-186-533
18 948 62.5 987 15 US-09-107-532-3319
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20 937 61.7 942 1 PCT-US02-03987-9823
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22 937 61.7 942 39 US-10-072-851-8823
23 937 61.7 948 15 US-09-134-000-1582
24 920 60.6 3656 14 US-09-070-927-577
25 920 60.6 3656 14 US-09-070-927A-577
26 863 56.9 547 17 US-09-308-397-5
27 858 56.5 1196 1 PCT-US97-07950-8
28 858 56.5 1199 12 US-08-832-030-78
29 858 56.5 1209 16 US-09-297-451-81
30 858 56.5 1209 16 US-09-297-451A-81
31 830 54.7 3627 48 US-60-045-649-929
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35 669.5 44.1 954 80 US-60-360-039-46809
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39 646 42.6 942 34 US-09-902-540-7357
40 646 42.6 5467 34 US-09-902-540-703
41 643.5 42.4 930 1 PCT-US02-03987-5028
42 643.5 42.4 930 31 US-09-815-242-8028
43 643.5 42.4 930 39 US-10-072-851-5028
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45 636 41.9 939 1 PCT-US02-03987-6878

ALIGNMENTS

RESULT 1
US-09-308-397-1
; Sequence 1, Application US/09308397
; GENERAL INFORMATION:
; APPLICANT: Gentry, Daniel R.
; APPLICANT: Lonsdale, John T.
; APPLICANT: Payne, David J.
; APPLICANT: Pearson, Stewart C.
; APPLICANT: Van Aller, Glenn
; TITLE OF INVENTION: Novel FabD
; FILE REFERENCE: P50593
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: US 60/308,397
; EARLIER FILING DATE: 1996-11-18
; EARLIER APPLICATION NUMBER: PCT/US97/20992
; EARLIER FILING DATE: 1997-11-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-308-397-1

Alignment Scores:
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Score: 1518.00 Matches: 306
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
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; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583.110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 1251
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-1251

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Pred. No.: 1.58e-141 Length: 921
Score: 1518.00 Matches: 306
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-308-397-2 (1-306) x US-09-583-110-1251 (1-921)

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QY 21 AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeu 40
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QY 41 GlyTyrAspLeuArgTyrLeuIleAspThrGluLysAspLysLeuAanGlnThrArgTyr 60
DB 121 GGTATGATTTGCGTTATCTCATCGATCGGAGGACAACTCAATCAGACCCGCTAT 180

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DB 181 ACGCAACAGCGATTCCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAGGCG 240

QY 81 TyrGlnProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaSer 100
DB 241 TATCAGCGCTGATATGGTCGCTGGTTGCTCTTCGAGATACTCTGCTTGGTGGCAAGC 300

QY 101 GlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyrMetGlu 120
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QY 161 ThrProAlaGlnIleValIleAlaGlyGluValValAlaValAspArgAlaValGluLeu 180
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QY 221 AspPheThrCysProLeuValGlyAanThrGluAlaAlaValMetGlnLysGluAspIle 240
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QY 241 AlaGlnLeuLeuThrArgGlnValLysGluProValaArgPheTyrGluSerIleGlyVal 260
DB 721 GCTCAGCTCTTGACGCGTCAGGTCAAGGAACCGTTCGTTTCTATGAAAGTATTGGGTC 780

QY 261 MetGlnGluAlaGlyLysSerAsnPheIleGlyProGlyLysValLeuSerGly 280
DB 781 ATGCAAGAGCAGCGCATAGCAACTTTATCGAGATTGACCGGGGAAAGTCTTTGTCAAGT 840

QY 281 PheValLysLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSerLeu 300
DB 841 TTTGTTAAAAAATGATCAAACTGCTCATTAGCTCATGTGGAAGATCAAGCGAGTTTA 900

QY 301 ValAlaLeuLeuGluLys 306
DB 901 GTAGCACATTTAGAAAAA 918

RESULT 3
US-09-752-069A-30
; Sequence 30, Application US/09752069A
; GENERAL INFORMATION:
; APPLICANT: Dougherty, Thomas J.
; APPLICANT: Pucci, Michael J.
; APPLICANT: Dougherty, Brian A.
; APPLICANT: Davidson, Daniel B.
; APPLICANT: Bruccoleri, Robert E.
; APPLICANT: Thanassi, Jane A.
; APPLICANT: Farmer II, Bennett T.
; TITLE OF INVENTION: NOVEL BACTERIAL GENES AND PROTEINS THAT ARE ESSENTIAL
; TITLE OF INVENTION: FOR CELL VIABILITY AND THEIR USES
; FILE REFERENCE: D0001NP
; CURRENT APPLICATION NUMBER: US/09/752,069A
; CURRENT FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/174,089
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 30
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-752-069A-30

Alignment Scores:
Pred. No.: 1.58e-141 Length: 921
Score: 1518.00 Matches: 306
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 29 Gaps: 0

US-09-308-397-2 (1-306) x US-09-752-069A-30 (1-921)

QY 1 MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg 20
DB 1 ATGACTAAACAGCGCTTTTATTTGCTGGTCAGGTGCCAGTATCTAGGATGGGACGG 60

QY 21 AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeu 40
DB 61 GATTTCTATGATCATGATCCGATGTTAAAGAAACGATTGATCGAGCGAGTCAGGTGCTC 120

QY 41 GlyTyrAspLeuArgTyrLeuIleAspThrGluGluAspLysLeuAanGlnThrArgTyr 60
DB 121 GGTATGATTTGCGTTATCTCATCGATCGGAGGACAACTCAATCAGACCCGCTAT 180

QY 61 ThrGlnProAlaIleLeuAlaThrSerValaIleTyrArgLeuGlnGluLysGly 80
DB 181 ACGCAACAGCGATTCCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAGGCG 240

QY 81 TyrGlnProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaSer 100

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/961,527
FILING DATE: 1997-10-30
APPLICATION NUMBER: US 60/029,960
FILING DATE: 1996-10-31
ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB340PDI
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 19702 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-158-844-7

Alignment Scores:
Pred. No.: 6,466-140 Length: 19702
Score: 1518.00 Matches: 306
Percent Similarity: 100.00% Conservative: 0
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US-09-308-397-2 (1-306) x US-10-158-844-7 (1-19702)

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Qy 21 AspPheTyrAspGlnTyrProLeuValLysGluThrIleAspArgAlaSerGlnValLeu 40
Db 17089 GATTTCATGATCAGTATCCGATTGTTAAAGAAAGATTGATCGAGCGAGCCAGGTGTC 17030

Qy 41 GlyTyrAspLeuArgTyrIleuLeuAspThrGluAspLysLeuAsnGlnThrArgTyr 60
Db 17029 GGTATGATTGGGTATCTCATCGATACGGAAGAGCAAACTCAATCAGACCCGCTAT 16970

Qy 61 ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuGlnGluLysGly 80
Db 16969 ACGCAACAGCCATTCTAGCGATTCGGTTGCTATCTACCGTTTATTCAGAAAGGCG 16910

Qy 81 TyrGlnProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaSer 100
Db 16909 TATCAGCCTGATATGTTGCTGTTGCTCTCTGGAAGATATCTGCTTGGTGAAGT 16850

Qy 101 GlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyValatTyrMetGlu 120
Db 16849 GCGCCCTTGATTTCGAAGATCGGTGCTTGGTAGCTAAGGTGGAGCCTATATGGA 16790

Qy 121 GluAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluVal 140
Db 16789 GAAGCGGCTCTGCTGATCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGTTC 16730

Qy 141 IleGluAlaCysGlnLysAlaSerGluLeuGlyValValThrProAlaAsnTyrAsn 160
Db 16729 ATTGAAGACCTCTCAAAAGCTTCTGAACCTTGGAGTGTACTCCAGCCAACTATAC 16670

Qy 161 ThrProAlaGlnIleValIleAlaGlyGluValValAlaValAspArgAlaValGluLeu 180
Db 16669 ACACCTGCACAAATCGTATTGTCGAGAAGTGGTTGCGAGTTGATCGAGCGTTGAACCT 16610

Qy 181 LeuGlnGluAlaGlyAlaLysArgIleIleProLeuLysValSerGlyProPheHisThr 200
Db 16609 TTGCAAGACGAGGTGCCAACCGCTTGATTCCTTTAAGGTGTGAGTCCCTTTCACACC 16550

Qy 201 AlaLeuLeuGluProAlaSerGlnLysLeuAlaGluThrLeuAlaGlnValSerPheSer 220
Db 16549 GCTCTCTCTGACCTGCTAGCCAGAACTAGCTGAACTCTAGCTCAGGTAAATTTTCA 16490

Qy 221 AspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluAspIle 240

Db 17155 ATGACTAAACAGCCCTTTTATTGCTGTCAGGTGCCAGTATCTAGGATGGGACGG 17096

1 MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg 20

Db 17155 ATGACTAAACAGCCCTTTTATTGCTGTCAGGTGCCAGTATCTAGGATGGGACGG 17096

Db 16489 GATTTCATGTCCTCTAGTGGCAATACAGAGCTGCTGTGATGCAAAAAGAGACATT 16430

Qy 241 AlaGlnLeuLeuThrArgGlnValLysGluProValArgPheTyrGluSerIleGlyVal 260

Db 16429 GCTCAGCTCTTACCGCTCAGGTCAAGGAACCGCTTCTGTTCTATGAAAGTATTGGGTC 16370

Qy 261 MetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGly 280

Db 16369 ATCRAAGACGAGCATATAGCACTTTATCGAGATTGGACCGGGGAAAGTCTTGTGAGT 16310

Qy 281 PheValLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSerLeu 300

Db 16309 TTTGTTAAAAAATTGATCAACTGCTCACTTAGCTCATGTGGAGATCAAGCGAGTTTA 16250

Qy 301 ValAlaLeuLeuGluLys 306

Db 16249 GTAGCACTTTTAGAAAAA 16232

RESULT 7
US-60-029-960-61/c
SEQUENCE 61. Application US/60029960
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 1649
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/029,960
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 19706 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-60-029-960-61

Alignment Scores:
Pred. No.: 6,466-140 Length: 19706
Score: 1518.00 Matches: 306
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 46 Gaps: 0

US-09-308-397-2 (1-306) x US-60-029-960-61 (1-19706)

Qy 1 MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg 20

Db 17155 ATGACTAAACAGCCCTTTTATTGCTGTCAGGTGCCAGTATCTAGGATGGGACGG 17096

QY 21 AspPheTyrAspGlnTyrProLeuValLysGluThrIleAspArgAlaSerGlnValLeu 40
|||
Db 17095 GATTTCATGATCAGTATCCGATTCTTAAGAAACGATTGATCGAGCGAGCCAGTGCTC 17036
|||
QY 41 GlyTyrAspLeuArgTyrLeuIleAspThrGluGluAspLysLeuAsnGlnThrArgTyr 60
|||
Db 17035 GGTATGATTTCGGTATCTCATCGATACGGAGAGACAACTCAATCAGCCCGCTAT 16976
|||
QY 61 ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnGluLysGly 80
|||
Db 16975 ACGCAACAGCCATTCAGCGACTTCGGTGTGATCTACCTCCGTTTATTCGAAAGAAAGGC 16916
|||
QY 81 TyrGlnProAspMetValAlaGlyLeuSerLeuGluTyrSerAlaLeuValAlaSer 100
|||
Db 16915 TATCAGCCTGATATGTTGCTGGTGTGCTCTTGAGAAATACTCTGCCCTTGCGCAAGT 16856
|||
QY 101 GlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyrMetGlu 120
|||
Db 16855 GCGCGCTGGATTGGAAGATCGGTTGCTTGGTAGCTAAGCGTGGAGCCTATATGGAA 16796
|||
QY 121 GluAlaIleProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluVal 140
|||
Db 16795 GAAGCGGCTCCGCTGACTCTGCGAAGATGGTAGCTTCTCAATACGCCAGTAGAGTCT 16736
|||
QY 141 IleGluGluAlaCysGlnLysAlaSerGluLeuGlyValValThrProAlaAsnTyrAsn 160
|||
Db 16735 ATTGAAGAAGCTCTGCAAAAGCTCTGAACCTTGGAGTGGTACTCCAGCCCACTATAAC 16676
|||
QY 161 ThrProAlaGlnIleValIleAlaGlyGluValValAlaValAspArgAlaValGluLeu 180
|||
Db 16675 ACACCTGCACAAATCGTCTATCTCGAAGAGTGGTTGCAGTTGATCGAGCGGTTGAACCT 16616
|||
QY 181 LeuGlnGluAlaGlyValAlaLysArgLeuIleProLeuLysValSerGlyProPheHisThr 200
|||
Db 16615 TTGCAAGAAGCAGGTGCCAAAGCTTGATCTCTTAAGGTGTCAGGTCCCTTTCCACACC 16556
|||
QY 201 AlaLeuLeuGluProAlaSerGlnLysLeuAlaGluThrLeuAlaGlnValSerPheSer 220
|||
Db 16555 GCTCTCTTGAACCTGCTAGCCAGAAACTAGCTGAAACTCTAGCTCAGGTAAAGTTTTC 16496
|||
QY 221 AspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluAspIle 240
|||
Db 16495 GATTTTACTGTCCCTAGTCGGCAATACAGNAGCTGCTGTGATGCCAAAGAGAGACAT 16436
|||
QY 241 AlaGlnLeuLeuThrArgGlnValLysGluProValArgPheTyrGluSerIleGlyVal 260
|||
Db 16435 GCTCAGCTCTGACCGCTCAGGTCAAGGAACCCGTTCGTTCATGAAAGTATTGGGCTC 16376
|||
QY 261 MetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGly 280
|||
Db 16375 ATGCAAGAAGCAGGCAATAGCAACCTTATCGAGATTGACCGGGGAAAGTCTTGTGAGGT 16316
|||
QY 281 PheValLysLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSerLeu 300
|||
Db 16315 TTGTTTAAAAAATTGATCAAACTGCTCATTAGCTCATGTGGAAGATCAAGCGAGTTTA 16256
|||
QY 301 ValAlaLeuLeuGluLys 306
|||
Db 16255 GTAGCACCTTTAGAAAAA 16238
|||

RESULT 8

US-09-752-069A-256
; Sequence 256, Application US/09752069A
; GENERAL INFORMATION:
; APPLICANT: Dougherty, Thomas J.
; APPLICANT: Pucci, Michael J.
; APPLICANT: Dougherty, Brian A.
; APPLICANT: Davison, Daniel B.
; APPLICANT: Brucoleri, Robert E.
; APPLICANT: Thanassi, Jane A.
; APPLICANT: Farmer II, Bennett T.
; TITLE OF INVENTION: NOVEL BACTERIAL GENES AND PROTEINS THAT ARE ESSENTIAL

; TITLE OF INVENTION: FOR CELL VIABILITY AND THEIR USES
; FILE REFERENCE: D0001NP
; CURRENT APPLICATION NUMBER: US/09/752,069A
; CURRENT FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/174,089
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 256
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-752-069A-256

Alignment Scores:
Pred. No.: 3,248-141 Length: 945
Score: 1515.00 Matches: 305
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.67% Mismatches: 0
Query Match: 99.80% Indels: 0
DB: 29 Gaps: 0

US-09-308-397-2 (1-306) x US-09-752-069A-256 (1-945)

QY 1 MetThrIleThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg 20
Db 1 ATGACTAAACAGCCCTTTTATTGCTGCTCAAGGTGCCAGTATCTAGGCGATGGACGG 60
|||
QY 21 AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeu 40
|||
Db 61 GATTTCTATGATCAGTATCCGATTGTTAAGAAACGATTGATCGAGCGAGTCAAGTGCTA 120
|||
QY 41 GlyTyrAspLeuArgTyrLeuIleAspThrGluGluAspLysLeuAsnGlnThrArgTyr 60
|||
Db 121 GGTATGATTTCGGTATCTCATCGATACGGAAGAACAACTCAATCAGACCCGCTAT 180
|||
QY 61 ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuGlnGluLysGly 80
|||
Db 181 ACCCAACCAAGCCATTCAGGACTTCGGTGTGCTATCTACCGTTTATTCGAAAGAAAGGC 240
|||
QY 81 TyrGlnProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaSer 100
|||
Db 241 TATCAGCCTGATATGTTGCTGGTGTGCTCTTGGAAGATACTCTCCCTTGGTGCAAGC 300
|||
QY 101 GlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyrMetGlu 120
|||
Db 301 GCGCGCTTGGATTGGAAGATCGGTTGCTTGGTAGCTAAGCGTGGAGCCTATATGGAA 360
|||
QY 121 GluAlaIleProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluVal 140
|||
Db 361 GAAGCGGCTCTGCTGACTCTGCAAGATGGTAGCAATCTCAATACGCCAGTAGAGTCT 420
|||
QY 141 IleGluGluAlaCysGlnLysAlaSerGluLeuGlyValValThrProAlaAsnTyrAsn 160
|||
Db 421 ATTGAAGAAGCCTGTCAAAAGCTTCTGAACCTGGAGTGGTACTCCAGCCCACTATAAC 480
|||
QY 161 ThrProAlaGlnIleValIleAlaGlyGluValValAlaValAspArgAlaValGluLeu 180
|||
Db 481 ACACCTGCACAAATCGTCTATGCTGAGAGAGTGGTTGCAAGTGTGATCGAGCGTGTGACT 540
|||
QY 181 LeuGlnGluAlaGlyAlaLysArgLeuIleProLeuLysValSerGlyProPheHisThr 200
|||
Db 541 TTGCAAGAAGCAGGTGCCAAAGCTTGATTCTCTTAAGGTGTCAGGTCCCTTTCCACACC 600
|||
QY 201 AlaLeuLeuGluProAlaSerGlnLysLeuAlaGluThrLeuAlaGlnValSerPheSer 220
|||
Db 601 TCTCTCTTGAACCTGCTAGCCAGAACTAGCTGAAACTCTGCTCAGGTAAAGTTTTC 660
|||
QY 221 AspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluAspIle 240
|||
Db 661 GATTTTACTGTCCCTAGTCGGCAATACAGAAAGCTGCTGTGATGCAAAAGAGGACAT 720
|||
QY 241 AlaGlnLeuLeuThrArgGlnValLysGluProValArgPheTyrGluSerIleGlyVal 260
|||

Db 721 GCTCAGCTCTTGACGGCTCAGGTCACAGGAACCGCTTCGTTCTTATCAAAAGTATTGGGTC 780
 QY 261 MetGlnGluAlaGlyIleSerAsnPhelIleGluIleGlyProGlyLysValLeuSerGly 280
 Db 781 ATCAAGAGACGAGCATAGCACTTATCGAGATTGGACCGGGAAGTCTTGTACAGT 840
 QY 281 PheValLysLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSerLeu 300
 Db 841 TTTGTTAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTTA 900
 QY 301 ValAlaLeuLeuGluLys 306
 Db 901 GTAGCACCTTTAGAAAAA 918

RESULT 9

PCT-US97-22578-43
 ; Sequence 43, Application PC/TUS9722578
 ; GENERAL INFORMATION:
 ; APPLICANT: Baltz, Richard H.
 ; APPLICANT: Burgett, Stanley G.
 ; APPLICANT: DeHoff, Bradley S.
 ; APPLICANT: Jaskunas Jr., Stanley R.
 ; APPLICANT: Mills, Bradley J.
 ; APPLICANT: Norris, Franklin H.
 ; APPLICANT: Peery, Robert B.
 ; APPLICANT: Rostock Jr., Paul R.
 ; APPLICANT: Skatrud, Paul L.
 ; APPLICANT: Smith, Michele C.
 ; APPLICANT: Rokey, Pamela K.
 ; APPLICANT: Young-Bellido, Michele
 ; TITLE OF INVENTION: Streptococcus Pneumoniae DNA Sequences
 ; NUMBER OF SEQUENCES: 228
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Eli Lilly and Company
 ; STREET: Lilly Corporate Center
 ; CITY: Indianapolis
 ; STATE: Indiana
 ; COUNTRY: U.S.
 ; ZIP: 46285

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US97/22578
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Webster, Thomas D.
 ; REGISTRATION NUMBER: 39,872
 ; REFERENCE/DOCKET NUMBER: X-11162
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 317-276-3334
 ; INFORMATION FOR SEQ ID NO: 43:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3580 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO

PCT-US97-22578-43
 Alignment Scores:
 Pred. No.: 1.63e-140 Length: 3580
 Score: 1515.00 Matches: 305
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.67% Mismatches: 0
 Query Match: 99.80% Indels: 0
 DB: 1 Gaps: 0

US-09-308-397-2 (1-306) x PCT-US97-22578-43 (1-3580)
 QY 1 MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyValaGlnThrLeuGlyMetGlyVal 20
 Db 718 ATGACTAAACAGCCCTTTTATTGCTGGTCAAGGTGCCAGATCTTAGGGATGGGACGG 777
 QY 21 AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeu 40
 Db 778 GATTTCATGATCAGTATCCGATTGTAAAGAAACGATTGATCGAGCGAGTCAGGTGCTA 837
 QY 41 GlyTyrAspLeuArgTyrLeuIleAspThrGluGluAspLysLeuAsnGlnThrArgTyr 60
 Db 838 GGTATGATTGGTTATCTCATCGATACGAAAGACAACTCAATCAGACCCGCTAT 897
 QY 61 ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnLysGly 80
 Db 898 ACGCAACGACCATCTTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAGGCG 957
 QY 81 TyrGlnProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaSer 100
 Db 958 TATCAGCCTGATATGGTTGCTGTTGCTCTCTGGAGATATCTCTGCTTGGTGGCAAGC 1017
 QY 101 GlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyrMetGlu 120
 Db 1018 GCGGCTTGCATTTTGAAGATGCGGTGCTGCTAGCTAAGCGTGGAGCCTATATGAA 1077
 QY 121 GluAlaAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluVal 140
 Db 1078 GAAGCGCTCCTGCTACTCTGCAAGATGTTAGCAGTCTCAATACGCCAGTAGAGGTC 1137
 QY 141 IleGluGluAlaCysGlnLysAlaSerGluLeuGlyValValThrProAlaAsnTyrAsn 160
 Db 1138 ATTGAAGAAGCCTGTCAAAAGCTTCTGAACCTTGGAGTGCTTACTCCAGCAACTATAAC 1197
 QY 161 ThrProAlaGlnIleValIleAlaGlyGluValValAlaValAspArgAlaValGluLeu 180
 Db 1198 ACACCTGCACAAATCGTCATTGCTGGAGAAGTGCTTGCAGTTGATCGAGCGTTGAAC 1257
 QY 181 LeuGlnGluAlaGlyAlaLysArgLeuIleProLeuLysValSerGlyProPheHisThr 200
 Db 1258 TTGCAAGAAGCAGGTGCCAAACCTTGATTCCTCTTAAGGTGTCAAGTCCCTTCACACC 1317
 QY 201 AlaLeuLeuGluProAlaSerGlnLysLeuAlaGluThrLeuAlaGlnValSerPheSer 220
 Db 1318 TCTCTCCTTGACCTGCTGCCAGAACTAGCTGAAACTCTGCTCAGTAACTTTTCA 1377
 QY 221 AspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluAspIle 240
 Db 1378 GATTTTACTTGTCCCTAGTCGCAATACAGAACTGCTGTGTGTCANAAAGAGACATT 1437
 QY 241 AlaGlnLeuLeuThrArgGlnValLysGluProValArgPheTyrGluSerIleGlyVal 260
 Db 1438 GCTCAGCTCTTGACGGCTCAGGTCAAGGAACCCGTTTCTTCTATGAAAGTATTGGGTC 1497
 QY 261 MetGlnGluAlaGlyIleSerAsnPhelIleGluIleGlyProGlyLysValLeuSerGly 280
 Db 1498 ATCAAGAGACGAGCATAGCAACTTATCGAGATTGGACCGGGAAGTCTTGTACAGT 1557
 QY 281 PheValLysLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSerLeu 300
 Db 1558 TTTGTTAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTTA 1617
 QY 301 ValAlaLeuLeuGluLys 306
 Db 1618 GTAGCACCTTTAGAAAAA 1635

RESULT 10

PCT-US02-03987-9482
 ; Sequence 9482, Application PC/TUS0203987
 ; GENERAL INFORMATION:
 ; APPLICANT: Elittra Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits

```
/ TITLE OF INVENTION: Proliferation
/ FILE REFERENCE: ELITRA.028VPC
/ CURRENT APPLICATION NUMBER: PCT/US02/03987
/ CURRENT FILING DATE: 2002-02-02
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ NUMBER OF SEQ ID NOS: 15811
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9482
/ LENGTH: 921
/ TYPE: DNA
/ ORGANISM: Streptococcus pneumoniae
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(921)
PCT-US02-03987-9482

Alignment Scores:
Pred. No.: 3,966-141 Length: 921
Score: 1514.00 Matches: 305
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.67% Mismatches: 0
Query Match: 99.74% Indels: 0
DB: 1 Gaps: 0

US-09-308-397-2 (1-306) x PCT-US02-03987-9482 (1-921)
QY 1 MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg 20
DB 1 ATGACTAAACAGCCCTTTTATTTGCTGTCAGAGTGCCTGATCATGAGGATGAGGACG 60
QY 21 AspPheTyrAspGlnTyrProLeuValLysGlnThrLeuAspArgAlaSerGlnValLeu 40
DB 61 GATTTCTATGATCATGATCCGATTGTCGAAGAAACGATTGATCGAGCGAGTCAGGTGCTA 120
QY 41 GlyTyrAspLeuArgTyrLeuLeuAspThrGluGlnAspLysLeuAsnGlnThrArgTyr 60
DB 121 GCTTATGATTGCGTTATCTCATCATGACGAGGACGACAACTCATGACCCGCTAT 180
QY 61 ThrGlnProAlaLeuLeuAlaThrSerValAlaLeuTyrArgLeuGlnGluGlyGly 80
DB 181 ACGCAACAGCCATTCTAGCGACTTCGGTTGCTATCTACCGCTTTATTGCAAGAAAGGCG 240
QY 81 TyrGlnProAspMetValAlaGlyLeuSerLeuGlyGlnTyrSerAlaLeuValAlaSer 100
DB 241 TATCAGCTGATATGGTTGCTGTTGCTTTGGAGAACTCTGCGCTTGGTGGCAAGC 300
QY 101 GlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyrMetGlu 120
DB 301 GCGCGCTTGGATTGGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGGCTATATGAA 360
QY 121 GluAlaAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluVal 140
DB 361 GAAGCGGCTCTGCTGATCTGGCAAGATGTAGCAGTTCTCAATACGCCAGTAGAGGTC 420
QY 141 IleGluGluAlaCysGlnLysAlaSerGluLeuGlyValValThrProAlaAsnTyrAsn 160
DB 421 ATTGAAGAAGCCTGTCAAAAGCTCTGAACCTTGAGTGGTTATCTCCAGCCACTATAAC 480
QY 161 ThrProAlaGlnIleValIleAlaGlyValValAlaValAlaAspArgAlaValGluLeu 180
DB 481 ACACCTGCACAAATCGTCAATGCTGGAGAGTGGTTGCGAGTTGATCGAGCGGTTGAACCT 540
QY 181 LeuGlnGluAlaGlyAlaLysArgLeuIleProLeuLysValSerGlyProPheHisThr 200
DB 541 TTGCAAGAAGCAGGTGCCAAACGCTTGATCTCTTAAGGTGTCAGGTCCTTTCACACC 600
QY 201 AlaLeuLeuGluProAlaSerGlnLysLeuAlaGlnThrLeuAlaGlnValSerPheSer 220
DB 601 GCTCTCTTGAACTGCTAGCAGAACTAGCTGAAACTCTAGCTCAGGTAGGTTTTC 660
QY 221 AspPheThrCysProLeuValGlyAsnThrGluAlaValMetGlnLysGluAspIle 240
DB 1 MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg 20
DB 1 ATGACTAAACAGCCCTTTTATTTGCTGTCAGAGTGCCTGATCATGAGGATGAGGACG 60
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BEST AVAILABLE COPY

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QY 21 AspPheTyrAspGlnTyrProIleVallysGluThrIleAspArgAlaSerGlnValLeu 40
Db 61 GATTTCATGATCAGTATCCGATTGTCAAGAAAGACGATTGATCGAGCGAGTCAGGTGCTA 120
QY 41 GlyTyrAspLeuArgTyrLeuIleAspThrGluAspLysLeuAsnGlnThrArgTyr 60
Db 121 GGTATGATTGGTTATCTCATCGATACGGAAGAGCAAACTCAATCAGACCCGCTAT 180
QY 61 ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnIlyGly 80
Db 181 ACGCAACCGCATTCAGACCTCGGTGTGCTATCTACCGTTTATTGCAAGAAAGGCG 240
QY 81 TyrGlnProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaSer 100
Db 241 TATCAGCGCTGATATGGTTGCTGTCTGTGAGAAATCTCTGCTTGGTGGCAAGC 300
QY 101 GlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaIleArgGlyAlaTyrMetGlu 120
Db 301 GCGCGCTTGGATTTCGAAGATCGGTTGCTTGGTAGCTAAACGGTGGAGCCTATATGGA 360
QY 121 GluAlaAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluVal 140
Db 361 GAAGCGGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 141 IleGluGluAlaCysGlnLysAlaSerGluLeuGluValValThrProAlaAsnTyrAsn 160
Db 421 ATTGAAGAGCGCTGTCAAAAGCTTCTGAACCTTGGAGTGGTGTACTCCAGCCAACTATAAC 480
QY 161 ThrProAlaGlnIleValIleAlaGlyGluValAlaValAlaAspArgAlaValGluLeu 180
Db 481 ACACCTGCACAAATCGCTCATTTGCTGAGAAAGTGGTTGCAAGTGTGATCGAGCGGTGAACCTT 540
QY 181 LeuGlnGluAlaGlyAlaLysArgLeuIleProLeuLysValSerGlyProPheHisThr 200
Db 541 TTGCAAGAGCGCTGTCAAAAGCTTCTGAACCTTGGAGTGGTGTACTCCAGCCAACTATAAC 600
QY 201 AlaLeuLeuGluProAlaSerGlnLysLeuAlaGluThrLeuAlaGlnValSerPheSer 220
Db 601 GCTCTCTTGAACCTGCTAGCCAGAACTAGCTGAAACTCTAGCTCAGGTAAAGTATTTTCA 660
QY 221 AspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluAspIle 240
Db 661 GATTTCATGCTTGTCCCTAGTGGCAATACAGAACTGCTGTGATGCAAAAGAGGACATT 720
QY 241 AlaGlnLeuLeuThrArgGlnValLysGluProValArgPheTyrGluSerIleGlyVal 260
Db 721 GCTCAGCTCTGACGCGTCAGGTCAAGGAACCGTTCGTTTCTATGAAAGTATTTGGGCTC 780
QY 261 MetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGly 280
Db 781 ATGCAAGAGCGCGCTATAGCAACTTATCGAGATTGGACCGGGGAAAGTTTTTGTGAGGT 840
QY 281 PheValLysLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSerLeu 300
Db 841 TTGTTTAAAAAATTGATCGAACTGCTCACTTAGCTCATGTGGAAGATCAACGCGAGTTTA 900
QY 301 ValAlaLeuLeuGluLys 306
Db 901 GTAGCACTTTAGAAAAA 918
```

RESULT 12

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US-10-072-851-9482
; Sequence 9482, Application US/10072851
; GENERAL INFORMATION:
; APPLICANT: Carr, Grant J.
; APPLICANT: Xu, H. Howard
; APPLICANT: Foulkes, J. Gordon
; APPLICANT: Zamudio, Carlos
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
```

```
; APPLICANT: Trawick, John D.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits
; TITLE OF INVENTION: Proliferation
; FILE REFERENCE: ELITRA.028A
; CURRENT APPLICATION NUMBER: US/10/072,851
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/387,636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9482
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(921)
; US-10-072-851-9482
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Alignment Scores:
Pred. No.: 3,96e-141 Length: 921
Score: 1514.00 Matches: 305
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.67% Mismatches: 0
Query Match: 99.74% Indels: 0
DB: 39 Gaps: 0
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US-09-308-397-2 (1-306) x US-10-072-851-9482 (1-921)
```

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QY 1 MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg 20
Db 1 ATGACTAAACACGCTTTTATTGTTGTCAGAGTGCCAGTATCTAGGATGGACGG 60
QY 21 AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeu 40
Db 61 GATTTCATGATCAGTATCCGATTGTCAAGAAACGATTGATCGAGCGAGTCAGTGCTA 120
QY 41 GlyTyrAspLeuArgTyrLeuIleAspThrGluGluAspLysLeuAsnGlnThrArgTyr 60
Db 121 GGTATGATTGGCTTATCTCATCGATACGGAAGAGCAAACTCAATCAGACCCGCTAT 180
QY 61 ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnIlyGly 80
Db 181 ACGCAACCGCATTCAGACCTCGGTGTGCTATCTACCGTTTATTGCAAGAAAGGCG 240
QY 81 TyrGlnProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaSer 100
Db 241 TATCAGCGCTGATATGGTTGCTGTGTTTGTCTTTGGAGAACTACTCTGCTTGGTGGCAAGC 300
QY 101 GlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyrMetGlu 120
Db 301 GCGCGCTTGGATTTCGAAGATCGGTTGCTCTGTAGTAAAGCGTGGAGCCTATATGGA 360
QY 121 GluAlaAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluVal 140
Db 361 GAAGCGGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 141 IleGluGluAlaCysGlnLysAlaSerGluLeuGluValValThrProAlaAsnTyrAsn 160
Db 421 ATTGAAGAGCGCTGTCAAAAGCTTCTGAACCTTGGAGTGGTGTACTCCAGCCAACTATAAC 480
QY 161 ThrProAlaGlnIleValIleAlaGlyGluValAlaValAlaAspArgAlaValGluLeu 180
Db 481 ACACCTGCACAAATCGCTCATTTGCTGAGAAAGTGGTTGCAAGTGTGATCGAGCGGTGAACCTT 540
QY 181 LeuGlnGluAlaGlyAlaLysArgLeuIleProLeuLysValSerGlyProPheHisThr 200
Db 541 TTGCAAGAGCGGTGCCAAACCGTTGATTCTTCTTAGAGTGTGAGTGTGCTTTCACACC 600
```

QY 201 AlaLeuLeuGluProAlaSerGlnLysLeuAlaGlnThrLeuAlaGlnValSerPheSer 220
DB 601 GCTCTCTTGAACCTGCTAGCCAGAACTAGCTGAAACTCTAGCTCAGGTAAGTTTTC 660
QY 221 AspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluAspIle 240
DB 661 GATTTCCTCTCCCTAGTCTGCGCAATACAGAAGCTGCTGTGATGCAAAAAGAGGACATT 720
QY 241 AlaGlnLeuLeuThrArgGlnValLysGluProValArgPheThrGluSerIleGlyVal 260
DB 721 GCTCAGCTCTTGAAGCGCTCAGGTCAGGAACCCGTTCTGTTTCTATGAAGATTATGGGGTC 780
QY 261 MetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGly 280
DB 781 ATGCAAGAGCAGGATCAAGCACTTTATCGAGATTGGACCGGGGAAAGTTTGTCTAGGI 840
QY 281 PheValLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSerLeu 300
DB 841 TTTGTTAAAAAATTGATCGAAGCTGCTCAGCTAGCTCATGTGGAAGATCAAGCGAGTTTA 900
QY 301 ValAlaLeuLeuGluLys 306
DB 901 GTAGCACATTTAGAAAAA 918
RESULT 13
US-60-068-175-555
; Sequence 555, Application US/60068175
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert E.
; APPLICANT: Corley, Neil C.
; APPLICANT: Russo, Frank D.
; APPLICANT: Hann, Amy L.
; APPLICANT: Heath, Joe D.
; APPLICANT: Finney, Gregory L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF STREPTOCOCCUS PNEUMONIAE
; NUMBER OF SEQUENCES: 1175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/068,175
; FILING DATE: HEREWITH
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PM-0009-2 P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-416
; INFORMATION FOR SEQ ID NO: 555:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9753 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: genomic DNA
; IMMEDIATE SOURCE:
; CLONE: SPN2C557
US-60-068-175-555
Alignment Scores:

Pred. No.: 6,914-140 Length: 9753
Score: 1514.00 Matches: 305
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.67% Mismatches: 0
Query Match: 99.74% Indels: 0
DB: 50 Gaps: 0
US-09-308-397-2 (1-306) x US-60-068-175-555 (1-9753)
QY 1 MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnThrLeuGlyMetGlyArg 20
DB 1234 ATGACATAAAACAGCCCTTTTATTTGCTGCTCAAGTGCCCACTATCTTAGGGATGGACGG 1293
QY 21 AspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluAspIle 40
DB 1294 GATTTCCTCTCCCTAGTCTGCGCAATACAGAAGCTGCTGTGATGCAAAAAGAGGACATT 1353
QY 41 GlyThrAspLeuArgThrGluAlaGlyLeuSerLeuGluAspLysLeuAsnGlnThrArgThr 60
DB 1354 GGTTCATGATTTCGCTTATCTCATCGATACGGAAGAGGACAAACTCAATCAGACCCGCTAT 1413
QY 61 ThrGlnProAlaIleLeuAlaThrSerValAlaIleThrArgLeuLeuGlnGlyLysGly 80
DB 1414 ACGCAACAGCCCATTTCTAGCGACTTCGGTTCCTATCTACCGTTTATTTCCAAAGAAAGGCG 1473
QY 81 TyrGlnProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaSer 100
DB 1474 TATCAGCCTGATATGTTGCTGTTTGTCTCTTGAGAACTACTCTGCTTGGTGCAAGC 1533
QY 101 GlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaThrMetGlu 120
DB 1534 GCGCCTTGGATTTCGAAGATCGGTTGCTTGGTAGTAAGCGTGGAAGCCCTATATGAA 1593
QY 121 GluAlaAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluVal 140
DB 1594 GAAGCGGCTCTGCTGACTCTGCGCAAGATGGTAGAGTTCTCAATACGCCAGTACAGGTC 1653
QY 141 IleGluGluAlaCysGlnLysAlaSerGluLeuGlyValValThrProAlaAsnThrAsn 160
DB 1654 ATTTGAAGAGCGCTGTCAAAAGCTTCTGAAGTGGAGTGGTTACTCCAGCCCAACTATAC 1713
QY 161 ThrProAlaGlnIleValIleAlaGlyGluValValAlaValAspArgAlaValGluLeu 180
DB 1714 ACCTTCGCAAAATCGTCATTGCTGGAAGTGGTTGCATGTCGAGCGGTTGAACCTT 1773
QY 181 LeuGlnGluAlaGlyAlaLysArgLeuIleProLeuLysValSerGlyProPheHisThr 200
DB 1774 TTGCAAGAGCAGGTGCCAAACGCTTGATTCTCTTAAGGTGTAGGTCCTTTCACACC 1833
QY 201 AlaLeuLeuGluProAlaSerGlnLysLeuAlaGlnThrLeuAlaGlnValSerPheSer 220
DB 1834 GCTCTCTTGAACCTGCTAGCCAGAACTAGCTGAACTCTAGCTCAGGTAAGTTTTC 1893
QY 221 AspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluAspIle 240
DB 1894 GATTTCCTCTCCCTAGTCTGCGCAATACAGAAGCTGCTGTGATGCAAAAAGAGGACATT 1953
QY 241 AlaGlnLeuLeuThrArgGlnValLysGluProValArgPheThrGluSerIleGlyVal 260
DB 1954 GCTCAGCTCTTGAAGCGCTCAGGTCAGGAACCCGTTCTGTTTCTATGAAGATTATGGGGTC 2013
QY 261 MetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGly 280
DB 2014 ATGCAAGAGCAGGATCAAGCACTTTATCGAGATTGGACCGGGGAAAGTTTGTTCAGGT 2073
QY 281 PheValLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSerLeu 300
DB 2074 TTTGTTAAAAAATTGATCGAAGCTGCTCAGCTAGCTCATGTGGAAGATCAAGCGAGTTTA 2133
QY 301 ValAlaLeuLeuGluLys 306
DB 2134 GTAGCACATTTAGAAAAA 2151

RESULT 14
US-60-061-998-494
Sequence 494, Application US/60061998
GENERAL INFORMATION:
APPLICANT: LAGACE, ROBERT E.
APPLICANT: CORLEY, NEIL C.
APPLICANT: RUSSO, FRANK D.
APPLICANT: HANN, AMY L.
APPLICANT: HEATH, JOE D.
APPLICANT: FINNEY, GREGORY L.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF STREPTOCOCCUS PNEUMONIAE
TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 797
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/061,998
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PM-0006-2P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 494:
SEQUENCE CHARACTERISTICS:
LENGTH: 5963 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: SPN1c499
US-60-061-998-494
Alignment Scores:
Pred. No.: 1,516-137 Length: 5963
Score: 1488.00 Matches: 302
Percent Similarity: 99.67% Conservativity: 1
Best Local Similarity: 99.34% Mismatches: 0
Query Match: 98.02% Indels: 1
DB: 50 Gaps: 0
US-09-308-397-2 (1-306) x US-60-061-998-494 (1-5963)
Qy 1 MetThrylsThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyLeuGlyMetGlyArg 20
Db 2919 ATGACTAAACACGCTTTTATTGCTGCTCAAGGTGCCAGTATCTAGGATGGACGG 2978
Qy 21 AspPheTyRaspGlnTyRproIleValLysGluThrIleAspArgAlaSerGlnValLeu 40
Db 2979 GATTTCATGATCAGTATCCGATGTTTAAAGAAACGATTGATCGAGCGAGTCAGTGTCTA 3038
Qy 41 GlyTyRaspLeuArgTyRLeuLeuAspThrGluGluAspLysLeuAsnGlnThrArgTyR 60
Db 3039 GGTTATGATTGGTTATCTCATCGATACGGAAGAGACAACTCAATCAGACCCGCTAT 3098
Qy 61 ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyRArgLeuLeuGlnGlyGly 80
Db 3099 ACGCAACACCGCATCTAGCGACTTCGGTGTGCTATCTACCGTTTATTGCAAGAAAAGGC 3158

Qy 81 TyrGlnProAspMetValAlaGlyLeuSerLeuGlyGluTyRSerAlaLeuValAlaSer 100
Db 3159 TATCAGCCTGATATGGTTGCTGCTGTTGTTGCTCTTTGAGATACTCTGCTTGGTGGCAAGC 3218
Qy 101 GlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyRMetGlu 120
Db 3219 GGCCTCTTGATTTTGAAGATGGGTTGCTTGGTAGCTAAGCGTGGAGCCCTATATGGAA 3278
Qy 121 GluAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluVal 140
Db 3279 GAAGCGCTCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTC 3338
Qy 141 IleGluGluAlaCysGlnLysAlaSerGluLeuGlyValValThrProAlaAsnTyRAsn 160
Db 3339 ATTGAAGAGCCCTGTCAAAAGCTTCTGAACCTGGAGTGGTGTACTCCAGCCCAACTAAC 3398
Qy 161 ThrPro-AlaGlnIleValIleAlaGlyGluValValAlaValAspArgAlaValGluLeu 180
Db 3399 ACACCTGGCACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAAC 3458
Qy 180 uLeuGlnGluAlaGlyAlaLysArgLeuLeuLeuLeuLysValSerGlyProPheHisTh 200
Db 3459 TTTGCAAGAGCAGGTGCCAAACGCTTGATTCCTTAAAGGTGTCAAGTCCCTTTCCACAC 3518
Qy 200 rAlaLeuLeuGluProAlaSerGlnLysLeuAlaGluThrLeuAlaGlnValSerPheSe 220
Db 3519 CTCTCTCTTGAACCTGCTAGCCAGAACTAGCTGAAACTCTGGCTCAGTAACTTTTC 3578
Qy 220 rAspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluAspI 240
Db 3579 AGATTTTACTTGTCCCTAGTCGCAATACAGAAGCTGCTGTGATCAAAAAGAGACAT 3638
Qy 240 eAlaGlnLeuLeuThrArgGlnValLysGluProValArgPheTyRLeuSerIleGlyVa 260
Db 3639 TGCTCAGCTCTTACCGCTCAGTCAAGGAACCCGTTCTCTTATGAAAGATTGGGT 3698
Qy 260 lMetGlnGluAlaGlyIleSerAsnPheLeuGluIleGlyProGlyLysValLeuSerGl 280
Db 3699 CATGCAAGAGCAGGCAATAGCAACTTTATCGAGATTGGACCGGGAAGTCTTGTTCAGG 3758
Qy 280 yPheValLysLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSerLe 300
Db 3759 TTTTGTAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAACGAGTTT 3818
Qy 300 uValAlaLeu 303
Db 3819 AGTAGCACTT 3828
RESULT 15
US-60-360-039-42057
Sequence 42057, Application US/60360039
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 42057
LENGTH: 927
TYPE: DNA
ORGANISM: Lactococcus lactis
US-60-360-039-42057
Alignment Scores:
Pred. No.: 1,536-94 Length: 927
Score: 1048.00 Matches: 209
Percent Similarity: 80.52% Conservativity: 40


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; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/265,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 37621
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-10-282-122A-37621
Alignment Scores:
Pred. No.: 1,93e-144 Length: 921
Score: 1515.00 Matches: 305
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.67% Mismatches: 0
Query Match: 99.80% Indels: 0
DB: 9 Gaps: 0
US-09-308-397-2 (1-306) x US-10-282-122A-37621 (1-921)
Qy 1 MetThrLysThrAlaPheAlaGlyGlnGlyValAlaGlnTyrLeuGlyMetGlyArg 20
Db 1 ATGACTAAACAGCCCTTTTATTGCTGTCAGAGTCCCAAGTATCTAGGATGGACGG 60
Qy 21 AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeu 40
Db 61 GATTCTCATGATCAGTATCCGATGTTTAAAGAACGATTGATCGACGAGTCAGGTGCTA 120
Qy 41 GlyTyrAspLeuArgTyrLeuIleAspThrGluAspLysLeuAsnGlnThrArgTyr 60
Db 121 GGTATGATTTGGTGTATCTCATCGATACCGAAGAACAACTCAATCAGACCCGCTAT 180
Qy 61 ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnLysGly 80
Db 181 ACGAACACGCCATCTAGGACATTCGGTGTCTATCTACCGTTATTGCAAGAAAGGC 240
Qy 81 TyrGlnProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaSer 100
Db 241 TATCAGCCTGATATGTTGTTGTTGCTCTTCGAGAACTACTCTCCCTGGTGGCAAGC 300
Qy 101 GlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaIleTyrArgGlyAlaTyrMetGlu 120
Db 301 GGCCTTGGATTTTGAAGATGCGTTGCTTGTAGCTAAGCTGAGCCTATATGGAA 360
Qy 121 GluAlaAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluVal 140
Db 361 GAAGCGCTCTGCTGACTCTGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGTGC 420
Qy 141 IleGluAlaCysGlnTyrAlaSerGluLeuGlyValValThrProAlaAsnThrAsn 160
Db 421 ATTGAAGACCTGTCAAAAGTTCTCGAACTGGAGTGTCTACTCCAGCCAACTATAAC 480
Qy 161 ThrProAlaGlnIleValIleAlaGlyGluValAlaValAspArgAlaValGluLeu 180
Db 481 ACACCTCCAAATCGTTCATTTGCTGGAGAGTGGTTGCAGTTGATCGAGCGGTGAAC 540
Qy 181 LeuGlnGluAlaGlyAlaLysArgLeuIleProLeuLysValSerGlyProPheIleThr 200
Db 541 TTGCAAGACGAGTGGCAACCGCTGATTCCTTAAAGGTGTCAGGTCCCTTTCACACC 600
Qy 201 AlaLeuLeuGluProAlaSerGlnLysLeuAlaGluThrLeuAlaGlnValSerPheSer 220
Db 601 TCCTCTCTGACCTGTCAGCAAGAACTAGCTGAACCTCTGGCTCAGTAGATTTCACA 660
Qy 221 AspPheThrCysProLeuValGlyAsnThrGluAlaValMetGlnLysGluAspIle 240
```

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Db 661 GATTTTACTTGTCCCTAGTCGCAATACAGAAAGTCTGTGATGCAAAAAGAGCATT 720
Qy 241 AlaGlnLeuLeuThrArgGlnValLysGluProValArgPheTyrGluSerIleGlyVal 260
Db 721 GCTCAGCTCTTGAGCGCTCAGGTCAAGAACCCGTTCTGTTCTATGAAGATTATGGGTC 780
Qy 261 MetGlnGluAlaGlyIleSerAsnPheIleGluLeuGlyProGlyLysValLeuSerGly 280
Db 781 ATGCAAGACGAGCATTAAGCAACTTTATCGAGATTGGACCGGGAAGTCTTGTCTAGGT 840
Qy 281 PheValLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSerLeu 300
Db 841 TTTGTTAAAAAATTGATCAACTGCTCACTTACCTGCTGATGGAAGATCAAGCGAGTTTA 900
Qy 301 ValAlaLeuLeuGluLys 306
Db 901 GTAGCACTTTTAGAAAAA 918
RESULT 2
US-10-282-122A-36004
; Sequence 36004, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 36004
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Streptococcus mutans
US-10-282-122A-36004
Alignment Scores:
Pred. No.: 5,44e-103 Length: 918
Score: 1109.00 Matches: 219
Percent Similarity: 83.33% Conservative: 37
Best Local Similarity: 71.80% Mismatches: 49
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Query Match: 72.99% Indels: 0
DB: 9 Gaps: 0
US-09-308-397-2 (1-306) x US-10-282-122A-36004 (1-918)
Qy 1 MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg 20
Db 1 ATGACAAAACACAGCATTTTATTGCTGGCCAGAGCTCAAAAACCTTGTGTATGGCAAGT 60
Qy 21 AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeu 40
Db 61 GATTGTATGAATTTTACCCAGTGTCAAGAGAGACTTTTAAACCCGCTCATTTCAATTTG 120
Qy 41 GlyTyrAspLeuArgTyrLeuIleAspThrGluAspLysLeuAsnGlnThrArgTyr 60
Db 121 GGTATGATGCTGCTTTGATTGATAATGATGAAGAAAGCTAAATCAACACGTTAT 180
Qy 61 ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuGlnGluLysGly 80
Db 181 GCACAGCCAGCGATTTTAAACAACTTCAGTACTATTATGCTCTTTTGAAGAAAGGAT 240
Qy 81 TyrGlnProAspMetValAlaGlyLeuSerLeuGlyGlnTyrSerAlaLeuValAlaSer 100
Db 241 TATCAACAGACATTTGCTGGACTGTCACTAGAGAACTACTCTGCTCTGTGTGACCC 300
Qy 101 GlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyrMetGlu 120
Db 301 GGTGCCATTTCAATTTGAAGATGCCTTAGCCCTTGCTGCAAAACGCTGGTGAATTTATGAA 360
Qy 121 GluAlaAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluVal 140
Db 361 ACACAGCACCCTGGTGGAGTGGGAAATGGTCTGTTATGAATATCTGCCCTTAGGCTC 420
Qy 141 IleGluGluAlaCysGlnLysAlaSerGluLeuGlyValValThrProAlaAsnTyrAsn 160
Db 421 ATTGAAGAGATTGTCAGAAAGCCAGCTCTAAAGGCAATGTTAGTCCAGCTAATTAAT 480
Qy 161 ThrProAlaGlnIleValIleAlaGlyGluValValAlaValAspArgAlaValGluLeu 180
Db 481 ACTCTACACAAATTTGTTATTGGTGGTGAAGTAGCAGCTGTTGATTATGCTGTGGAACTT 540
Qy 181 LeuGlnGluAlaGlyAlaLysArgLeuIleProLeuLysValSerGlyProPheHisThr 200
Db 541 TTAAAGGAGCTGGTAGTAACGTTTGATTCTCTTAAGTTTCTGCTCCCTTTTCATCG 600
Qy 201 AlaLeuLeuGluProAlaSerGlnLysLeuAlaGlnThrLeuAlaGlnValSerPheSer 220
Db 601 GCTCTTTTGAATCTGCTAGTCAAAAATGGCTCAAGCTTTGGAATAATTAATAATTTTCA 660
Qy 221 AspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluAspIle 240
Db 661 GATTTCATGCTTCCACTAGTGGGAACTAAAGCTGAATTAAGAGAAACAGGAGATT 720
Qy 241 AlaGlnLeuLeuThrArgGlnValLysGluProValArgPheTyrGluSerIleGlyVal 260
Db 721 AAAACCTTTGCTGCTCGTCAAGTCAAGAAACCTGTTGCTCTTCTATGAATCTATTGCTGTA 780
Qy 261 MetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGly 280
Db 781 ATGCAAAAATTTGGTGTGAATAACTATGTCGAAATTTGACCTGGTGAAGGCTTTCAGTGGT 840
Qy 281 PheValLysLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSerLeu 300
Db 841 TTTGTGAAAAGATTGATAATCTGCAAGATCTCAGCTGTTGGAAGCTTAGCTAGTTG 900
Qy 301 ValAlaLeuLeuGlu 305
Db 901 CAGGCTTTCTTAGAT 915
```

RESULT 3

US-10-369-493-42057

; Sequence 42057, Application US/10369493

; GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 42057
LENGTH: 927
TYPE: DNA
ORGANISM: Lactococcus lactis
US-10-369-493-42057

Alignment Scores: 7.12e-97 Length: 927
Pred. No.: 1048.00 Matches: 208
Score: 1048.00
Percent Similarity: 80.52% Conservative: 40
Best Local Similarity: 67.53% Mismatches: 58
Query Match: 69.04% Indels: 2
DB: 8 Gaps: 1

US-09-308-397-2 (1-306) x US-10-369-493-42057 (1-927)

```
Qy 1 MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg 20
Db 1 ATGACAAAACACAGCATTTTATTGCTGGCCAGAGCTCAAAAACCTTGTGTATGGCAAGT 60
Qy 21 AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeu 40
Db 61 GACTTATATGACCAATATGAAACAGTTAAAGCAACTTTTTCATGAAGCAAGTCAAGCTTTA 120
Qy 41 GlyTyrAspLeuArgTyrLeuIleAspThrGluGluAspLysLeuAsnGlnThrArgTyr 60
Db 121 GGATATGATTTGCGAGCTTTGATTGATATGATGAAGAAACCTAATGAACAAAGTAC 180
Qy 61 ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuGlnGluLysGly 80
Db 181 ACTCAACCTGCAATTTTAAACACCTCTGTTGCTATTTTACGTTTGTAAAGTGAAGTGG 240
Qy 81 TyrGlnProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaSer 100
Db 241 ATTAAACCTGACCTTGTCTGCTGCTTGTAGTCTTGTGAATATCTGCTTGTGTAGCATCA 300
Qy 101 GlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyrMetGlu 120
Db 301 GGNATCATTTGATTTTCAAGAGCAGTTAAGCTTGTAGCTAAACGTTGTCATATATGACA 360
Qy 121 GluAlaAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluVal 140
Db 361 GAAGCTGCACCCAGCTGTTCTGTTAAATGGTCTGTTAATGAACACAGACCCAGCCTTG 420
Qy 141 IleGluGluAlaCysGlnLysAlaSerGluLeu-----GlyValValThrProAlaAsn 158
Db 421 ATTGAAGAAATTTGCCAGAAAGCCGCGCAATTTAAAGCGGATATTGTAGTCCAGCAAT 480
Qy 159 TyrAsnThrProAlaGlnIleValIleAlaGlyGluValValAlaValAspArgAlaVal 178
Db 481 TATAACACGCCCGCACAAATTTGTTATGGTGGTGAAGTTGAGCGGCTTGATTATGCTGTT 540
Qy 179 GluLeuLeuGlnGluAlaGlyAlaLysArgLeuIleProLeuLysValSerGlyProPhe 198
Db 541 GAGTTCTTAAAGAACCCGAGTTCTGTAACCTTTATGAATTTAAAGTTTCAGAGCCTTTC 600
Qy 199 HisThrAlaLeuLeuGluProAlaSerGlnLysLeuAlaGlnThrLeuAlaGlnValSer 218
Db 601 CATACAGCAATTTTAAACACGAGCATCTGAAAAATTTGGCTTTGGAGCTTGTATAAATTTGAT 660
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Qy 219 PheserAspPheThrCysProLeuValGlyAsnThrGluAlaValMetGlnLysGlu 238
Db 661 TTTAGACCTTTTGAATACCAATTAATCTCAATACAGTCTAAAGTAATGGAATGAT 720
Qy 239 AspIleAlaGlnLeuLeuThrArgGlnValLysGluProValArgPheTyrGluSerIle 258
Db 721 GAAGTCAAGGACTTTTGACCGCTCAAGTCATCGACCACTGCTTTTATGAATCGGT 780
Qy 259 GlyValMetGlnGluAlaGlyIleSerAsnPhelIleGluIleGlyProGlyLysValLeu 278
Db 781 GAAACAATGCAAAACTAGGGGGGCACTCGCTTTTATTGAAGTTGGTCTCTGGAGTACTT 840
Qy 279 SerGlyPheValLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAla 298
Db 841 TCAGGTTTCATTAATAAATGTAATAATGCAGAAATGCTAAATGTTGAAAATTTAGCT 900
Qy 299 SerLeuValAlaLeuLeuGluLys 306
Db 901 TCATTTGAAGCTTTGATTATATCAG 924

RESULT 4
US-10-282-122A-38525
; Sequence 38525, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Orlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EUTRA.0344
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38525
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
US-10-282-122A-38525

Alignment Scores:
Pred. No.: 1,21e-95 Length: 939
Score: 1036.00 Matches: 209
Percent Similarity: 81.05% Conservative: 39

Best Local Similarity: 68.30% Mismatches: 58
Query Match: 68.25% Indels: 0
DB: 9 Gaps: 0
US-09-308-397-2 (1-306) x US-10-282-122A-38525 (1-939)

Qy 1 MetThrIysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg 20
Db 1 ATGCAAGACAGCCTTTTATTTCGCGTCAAGGTCTCAAAATTTAGGATGGCAAGG 60
Qy 21 AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeu 40
Db 61 GATTTTATGATACTTTGCTATTGTAAAGAAAAACCTTTGATCAAGCTAGTCAAGTATTG 120
Qy 41 GlyTyrAspLeuArgTyrLeuIleAspThrGluGluAspLysLeuAsnGlnThrArgTyr 60
Db 121 GGATACGATTTCGCCCTTTGATTGATGATGACAGTTAAACTTAATCAACATAGCTAT 180
Qy 61 ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnLysGly 80
Db 181 ACGCAACGAGCTATTTTGACATCATCAATTGCTATTATTACCGTGTGTTGGGCTTACATCAC 240
Qy 81 TyrGlnProAspMetValAlaGlyLeuSerLeuGlyClnTyrSerAlaLeuValAlaSer 100
Db 241 GTTAAACCGGATATGGTAGCTGCTTTCCTTAGGAGATACACTCAGCTTTGGTAGCATCA 300
Qy 101 GlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyrMetGlu 120
Db 301 GGGGCACTCTTTTGAAGATACCTTATCTTAGTAGTAAGAGAGCCGCTTGATGGAG 360
Qy 121 GluAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluVal 140
Db 361 GAAGCAGCACCAAGGATCTGGAAGATGTTGCCGTTATGATATACAGACGTCGAAGTC 420
Qy 141 IleGluGluAlaCysGlnLysAlaSerGluLeuGlyValValThrProAlaAsnTyrAsn 160
Db 421 ATCGAAGAGTCTGCTCAATAGCTGCTAAACATGGAGTGGTGTCTCCAGCAAACTATAAT 480
Qy 161 ThrProAlaGlnIleValIleAlaGlyGluValValAlaValAspArgAlaValGluLeu 180
Db 481 ACTCCTAGTCAAAATGTAATTTGGTGGTCAGACAGATCTGTGAACGTGGCAGTTGAACCTT 540
Qy 181 LeuGlnGluAlaGlyAlaLysArgLeuIleProLeuLysValSerGlyProPheHisThr 200
Db 541 TTAAGGAAAGGGAGTAAAGCTTTAATCCCTTTAAACGTGTCAGTCTCTTCCACT 600
Qy 201 AlaLeuLeuGluProAlaSerGlnLysLeuAlaGluThrLeuAlaGlnValSerPheSer 220
Db 601 GCTTTGTAGAACCCAGCTAGCGCTTGTGGCTAAAGAGTTGGAAGATACACACTCAGT 660
Qy 221 AspPheThrCysProLeuValGlyAsnThrGluAlaValMetGlnLysGluAspIle 240
Db 661 GACTTCAAGATTCCTTTGGTTGGTAATACCGAAGCTAATATTATGGAAGAACCCGTATC 720
Qy 241 AlaGlnLeuLeuThrArgGlnValLysGluProValArgPheTyrGluSerIleGlyVal 260
Db 721 CCAGACTATTAGCCCGCTCAAGTCAATGGAGCTGCTGTTTATGACAGTGTTCGCACT 780
Qy 261 MetGlnGluAlaGlyIleSerAsnPhelIleGluIleGlyProGlyLysValLeuSerGly 280
Db 781 TTAGTAGAAGTGGCATAACACAATTCATTGAGTAGGACGACGAGTAAAGTTTTCACAGGT 840
Qy 281 PheValLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSerLeu 300
Db 841 TTTGTGAAGAAATGATAAAATTTACTATGTTACTAGTGTGTTGAACATCGTAAAGCTTA 900
Qy 301 ValAlaLeuLeuGluLys 306
Db 901 CGTTTATTTTAGATAGA 918

RESULT 5
US-10-282-122A-21491
; Sequence 21491, Application US/10282122A

APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3319:
SEQUENCE CHARACTERISTICS:
LENGTH: 987 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...987
SEQUENCE DESCRIPTION: SEQ ID NO: 3319:
US-10-417-884-3319

Alignment Scores:

Pred. No.: 1,18e-86 Length: 987
Score: 948.00 Matches: 188
Percent Similarity: 78.03% Conservative: 50
Best Local Similarity: 61.64% Mismatches: 63
Query Match: 62.45% Indels: 4
DB: 8 Gaps: 2

US-09-308-397-2 (1-306) x US-10-417-884-3319 (1-987)

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Qy 3 LysThrAlaPheLeuPheLeuGlyGlnGlyValGlnTyrLeuGlyMetGlyArgAspPhe 22
Db 73 AAACAGCATCTTATTAGTGGCCAAAGTGCACATATACAGGTATGCGAAAGATTATA 132
Qy 23 TyrAspGlnTyrProLeuValLysGluThrLeuAspArgAlaSerGlnValLeuGlyTyr 42
Db 133 TATCAAGAA---GCCGTTGTAAAGCAGACATTTGATGAAGCAAGTGAGATTCTCGGCTAC 189
Qy 43 AspLeuArgTyrLeuLeuAspThrGluGluAspLysLeuAsnGlnThrArgTyrThrGln 62
Db 190 GATATGCTGAACTTTGCTTTTACAGAAATGAACGTTTGATCAGACGCAATATACAG 249
Qy 63 ProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnGlnLysGlyTyrGln 82
Db 250 CCAGCTATTCTAACAGTCAGCATCGCGTATTATCGCTTATTGAAGGAGCATGGAATCATC 309
Qy 83 ProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaSerGlyAla 102
Db 310 CCAGATGCAGCTTTAGACGTCAGTTTAGAGAAATATTCGCGATTAGTAGTAGTAATGCG 369
Qy 103 LeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyrMetGluGluAla 122
Db 370 CTATCTTCACTGAACGAGTTGCTTAGTAGCAAAAGAGGCGCTTATATGACAGAAGCT 429
Qy 123 AlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluValIleGlu 142
Db 430 ACCCCAGCTGGAAGCGGAAATGGTTGCAGTGATGAATGCCCGGATTGAAACGATCGAG 489
Qy 143 GluAlaCysGlnLysAlaSerGluLeuGlyValValThrProAlaAsnTyrAsnThrPro 162
Db 490 GAAGCTGTCATGAGCTAGCAGTAGCGGATCGTATCTCTGCAATTTATATACACT 549
Qy 163 AlaGlnIleValIleLeuGlyGluValAlaValAlaAspArgAlaValGluLeuGln 182
Db 550 CAGCAGATCGTATGTTGTCGCGAAGAAAGCAGTAGAGCAGCTGTTTACTATTATAAA 609
```

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Qy 183 GluAlaGlyAlaLysArgLeuLeuProLeuLysValSerGlyProPheHisThrAlaLeu 202
Db 610 GAAAAGGGTTCAAAAAGATGATCCCTCTAAATGTGAGCGGCCCTTTTTCATACAGTATT 669
Qy 203 LeuGluProAlaSerGlnLysLeuAlaGluThrLeuAlaGlnValSerPheSerAspPhe 222
Db 670 TTAGAACCAGCAGCAAAAACATGGCGAAGGACCTTAAGTCAGATTCATCTCTGACCT 729
Qy 223 ThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluAspIleAlaGln 242
Db 730 TCTTTCTTATCATAAAGCAACACCAACGGAATAATGAAGAAAGAAACAATCGCGGGA 789
Qy 243 LeuLeuThrArgGlnValLysGluProValArgPheTyrGluSerIleGlyValMetGln 262
Db 790 CTACTTGAACAGCAAGTCATGCAACTGTTCTGTTTCTATGAGAGTATCCATAGTTAA 849
Qy 263 GluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGlyPheVal 282
Db 850 ACAATCGCATCGAACCAAGTCATCGAAGTCGCGCCGCGAAAGTATTAAGCGGATTATG 909
Qy 283 LysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSerLeu----- 300
Db 910 AAAAAATCGATAAAACAATACCAGTTCTCGGTGTTGAGAATAAGCAGACATTTGATGAA 969
Qy 301 ---ValAlaLeuLeu 304
Db 970 ACAATAGCAATACTA 984
RESULT 7
US-10-282-122A-20712
; Sequence 20712, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EUIPA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20712
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```
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-282-122A-20712

Alignment Scores:
Pred. No.: 1.44e-85 Length: 927
Score: 937.00 Matches: 187
Percent Similarity: 75.17% Conservative: 40
Best Local Similarity: 61.92% Mismatches: 75
Query Match: 61.73% Indels: 0
DB: 9 Gaps: 0

US-09-308-397-2 (1-306) x US-10-282-122A-20712 (1-927)

QY 3 LysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArgAspPhe 22
DB 4 AAAACAGCGATTTATTAGTGGACAAAGGACCCAGTATCAAGGGATGGGTGAAGAATTA 63
QY 23 TyrAspGlnTyrProIleValIysGluThrIleAspArgAlaSerGlnValLeuGlyTyr 42
DB 64 TATCACCAGAGCGATTTGTCGGAAACCTTCGATGAGCAAGTCATATCTTAGTTAT 123
QY 43 AspLeuArgTyrLeuIleAspThrGluGluAspLysLeuGlnThrArgTyrThrGln 62
DB 124 GAGATGGCAGAACTTTGTTTACTGAAATGAACGTTTAAATGAACAGATATACGAA 183
QY 63 ProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnGlyLysGlyTyrGln 82
DB 184 CTGCTGATTTTAAACGTACGTGTCGATTTTACCGTCTTTTGCAACAAAGGACTAAGC 243
QY 83 ProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaSerGlyAla 102
DB 244 CTGATGTCGTAGCGGGTTTAAGCTTAGCGGAATACAGTGTCTTGGTTGCGAGCGGGCT 303
QY 103 LeuAspPheGluAspAlaValAlaLeuValAlaIleTyrMetGluGluAla 122
DB 304 TTGCGCTTTTCAGAGCAGTGGCTTGGTCCAAAGCGCGTCACTGATGACAGAGCA 363
QY 123 AlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluValIleGlu 142
DB 364 GCACCAACAGGAACTGGCAAAATGTTCTGTTATGATGCTGAGCGGTGAAGTAATTGAG 423
QY 143 GluAlaCysGlnLysAlaSerGluLeuGlyValValThrProAlaAsnTyrAsnThrPro 162
DB 424 AAAGCCTGCCAAGAGCAGCGTCTTTCGSAATTTGGCTCCAGCAAAATTAATATACCA 483
QY 163 AlaGlnIleValIleAlaGlyGluValValAlaValAspArgAlaValGluLeuGln 182
DB 484 CAACAAATCGTGATTTGGTGGTGGTCTGCTGCTGTGATCAAGCGATGACACTTCTCAA 543
QY 183 GluAlaGlyAlaLysArgLeuIleProLeuLysValSerGlyProPheHisThrAlaLeu 202
DB 544 GAAGCTGGTGTGAGCGAATGATTCGTTAAATGTGAGTGGCCCTTTCCATACGCGCGTG 603
QY 203 LeuGluProAlaSerGlnLysLeuAlaGlnThrLeuAlaGlnValSerPheSerAspPhe 222
DB 604 TTACACCAAGCATCAAAATAATGGCTCAGATTTAGCAAAATTTGAACCTTTCAACCGATG 663
QY 223 ThrCysProLeuValGlyAsnThrGluAlaValMetGlnLysGluAspIleAlaGln 242
DB 664 CAATTCCTGTCTATTAGTAATACGACTGCCGAAATATTGCCCAAGAGCGCAATCAAGCG 723
QY 243 LeuLeuThrArgGlnValIysGluProValArgPheTyrGluSerIleGlyValMetGln 262
DB 724 TTATTGAAAGCAAGTCAATGCTCGGTACGTTTGAAGACAGTATCGAAACGATGAAG 783
QY 263 GluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGlyPheVal 282
DB 784 GCTATCAACCTAGGACGATGATTGAGTTGCTCCAGGGAAACATTAATTAATTAATTA 843
QY 283 LysLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSerLeuValAla 302
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Db      562 GAAGCTGGTGAAGCGAATGATTCGGTTAAATGTGAGTGGCCCTTCCATACGGCGCTG 621
Qy      203 LeuGluProAlaSerGlnLysLeuAlaGluThrLeuAlaGlnValSerPheSerPhe 222
Db      622 TTAACACCGATCAAAAATTTGGCTCAGGATTTAGCAAAATTTGAACTTTCAACGATG 681
Qy      223 ThrCysProLeuValGlyAsnThrGluAlaValMetGlnLysGluAspIleAlaGln 242
Db      682 CAATTCCTGTCATTAGTAATACGACTGCCGAAATTTATGCCCAAGAGCAATTTCAAGCG 741
Qy      243 LeuLeuThrArgGlnValLysGluProValArgPheTyrGluSerIleGlyValMetGln 262
Db      742 TTATTGAAAGCAAGTCATGCTGCGGTACGTTTTCAGACACATATCGAAACGATGAAG 801
Qy      263 GluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGlyPheVal 282
Db      802 GCTATGAACGTAGGAACGATGATGAAGTTGGTCCAGGGAACATTAATCTGTTTGT 861
Qy      283 LysLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSerLeuValAla 302
Db      862 AAAAAAATTGCAAAACAAATTTGAATGACCCGCTGGTGAAGATGTTGCAACATTAACAG 921
Qy      303 LeuLeu 304
Db      922 ACGTTA 927

RESULT 9
US-09-134-000C-1582
; Sequence 1582, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1582
; LENGTH: 948
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1582

Alignment Scores:
Pred. No.: 1,48e-85 Length: 948
Score: 937.00 Matches: 187
Percent Similarity: 75.17% Conservative: 40
Best Local Similarity: 61.92% Mismatches: 75
Query Match: 61.73% Indels: 0
DB: 6 Gaps: 0

US-09-308-397-2 (1-306) x US-09-134-000C-1582 (1-948)
Qy      3 LysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArgAspPhe 22
Db      22 AAAAAACGATTTATTAGTGACAAGGAGCCGAGTATCAAGGGATGGGTGAAGAATTA 81
Qy      23 TyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeuGlyTyr 42
Db      82 TATCACCACAAGCGATTTGTCGGGAACTTCGATGAAGCAAGTATCATCTTAGTTAT 141
Qy      43 AspLeuArgTyrIleuLeuAspThrGluGluAspLysLeuAsnGlnThrArgTyrThrGln 62
Db      142 GAGATGCCAGCACTTTGTTTACTGAAATGAACGTTTAAATGAAACAGATATACGCAA 201
Qy      63 ProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnGluLysGlyTyrGln 82
Db      202 CCTGCTATTATAACGTCAGTGTGCGCATTTTACCGCTTTTGGCAACAAAAGAGCAATACG 261

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Qy      83 ProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaSerGlyAla 102
Db      262 CCTGATCTGTAGCGGCTTTAAGCTTAGGGGAATACAGTGCCTTTGGTTGCACGGGGCT 321
Qy      103 LeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyrMetGluGluAla 122
Db      322 TTGGCTTTTCAGAGCAGTGGCTTGGTCCAAAAGCGCGTCAGTACATGACAGAAGCA 381
Qy      123 AlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluValIleGlu 142
Db      382 GCACCACAAGAACTGCCAAAATGCTGCTTATGAATGCTGAGCGTGAAGTAATTTAG 441
Qy      143 GluAlaCysGlnLysAlaSerGluLeuGlyValValThrProAlaAsnTyrAsnThrPro 162
Db      442 AAGCCCTCCAGAGCAAGTGGTTCGGAATTTGGTCCAGCAAAATTAATATACACCA 501
Qy      163 AlaGlnIleValIleAlaGlyGluValValAlaValAspArgAlaValGluLeuGln 182
Db      502 CAACAAATCGTATGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 561
Qy      183 GluAlaGlyAlaLysArgLeuIleProLeuLysValSerGlyProPheHisThrAlaLeu 202
Db      562 GAAGCTGGTGAAGCGCAATGATTCGTTAAATGTGAGTGGCCCTTTCCATACGGCGCTG 621
Qy      203 LeuGluProAlaSerGlnLysLeuAlaGluThrLeuAlaGlnValSerPheSerAspPhe 222
Db      622 TTACACACGATCAAAAAAATTTGGCTCAGGATTTAGCAAAATTTGAACCTTTCAACCATG 681
Qy      223 ThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluAspIleAlaGln 242
Db      682 CAATTCCTGTCATTAGTAATACGACTGCCGAAATTTATGCCCAAGAGCAATTTCAAGCG 741
Qy      243 LeuLeuThrArgGlnValLysGluProValArgPheTyrGluSerIleGlyValMetGln 262
Db      742 TTATTGAAAGCAAGTCATGCTGCGGTACGTTTGAACACAGTATCGAAACGATGAAG 801
Qy      263 GluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGlyPheVal 282
Db      802 GCTATGAACGTAGGAACGATGATGAAGTTGGTCCAGGGAACATTAATCTGTTTGT 861
Qy      283 LysLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSerLeuValAla 302
Db      862 AAAAAAATTGCAAAACAAATTTGAATGACCCGCTGGTGAAGATGTTGCAACATTAACAG 921
Qy      303 LeuLeu 304
Db      922 ACGTTA 927

RESULT 10
US-10-434-665-1582
; Sequence 1582, Application US/10434665
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: PATH03-09
; CURRENT APPLICATION NUMBER: US/10/434,665
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: US 09/134,000
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1582
; LENGTH: 948
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-434-665-1582

Alignment Scores:
Pred. No.: 1,48e-85 Length: 948
Score: 937.00 Matches: 187

```


Percent Similarity: 75.17% Conservative: 40
Best Local Similarity: 61.92% Mismatches: 75
Query Match: 61.73% Indels: 0
DB: 8 Gaps: 0

US-09-308-397-2 (1-306) x US-10-434-665-1592 (1-948)

```
QY 3 LysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArgAspPhe 22
DB 22 AAAACAGCGATTATTTAGTGGACAGAGAGCCAGTATCAAGGATGGGTGAAGAATTA 81
QY 23 TyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeuGlyTyr 42
DB 82 TATCAACAAAGACGATTGTCGGAAACTTTCCGATGAAGCAAGTCATATCTTAGTTAT 141
QY 43 AspLeuArgTyrLeuIleAspThrGluAlaAspLysLeuAsnGlnThrArgTyrThrGln 62
DB 142 GAGATGGCAGAACTTTGTTTACTGAAATGAACGTTTAAATGAACAGATATACGGAA 201
QY 63 ProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnGlyLysGlyTyrGln 82
DB 202 CTGCTATTTTAAACAGTCAGTCGCACTTTTACCGCTTTTGCACAAAAGGACTAAGC 261
QY 83 ProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaSerGlyAla 102
DB 262 CTGATGTCGTAGCGGGTTTAACTTAGGGAAATACAGTCTTTGTTGCCAGCGGGCT 321
QY 103 LeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyrMetGluGluAla 122
DB 322 TTGCGGTTTTCAGAACGATGTCCTTGGTCCAAAGCGGGTCAGTACATGACAGAAGCA 381
QY 123 AlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluValIleGlu 142
DB 382 GCACCAAGAACTGCGAAAATGGTGTCTTATCAATGCTGAGCGTGAAGTAATTGAG 441
QY 143 GluAlaCysGlnLysAlaSerGluLeuGlyValValThrProAlaAsnTyrAsnThrPro 162
DB 442 AAAGCTGCGAAGAACCCAGTCTTCGGAATGTGGTCCAGCAAAATTAATACACA 501
QY 163 AlaGlnIleValIleAlaGlyGluValValAlaValAlaAspArgAlaValGluLeuGln 182
DB 502 CAACAAATCGTATTGGTGGTGAGGTTGCTGCTGTGTGATCAAGCGATGACACTTCTCAA 561
QY 183 GluAlaGlyAlaLysArgLeuIleProLeuLysValSerGlyProPheHisThrAlaLeu 202
DB 562 GAAGCTGGTGTGAAGCGAATGATCCGTTAAATGTGAGTGGCCCTTTCATACGCGCTG 621
QY 203 LeuGluProAlaSerGlnLysLeuAlaGluThrLeuAlaGlnValSerPheSerAspPhe 222
DB 622 TTACACACGATCAAAAATTTGGTTCAGGATTTAGCAAAATTCGAATTTCAAACGATG 681
QY 223 ThrCysProLeuValGlyAsnThrGluAlaIleValMetGlnLysGluAspIleAlaGln 242
DB 682 CAAATTCCTGTCAATAGTATACGATGCGCAAAATTTATGCCCAAGAGGCAATTCACGCG 741
QY 243 LeuLeuThrArgGlnValLysGluProValArgPheTyrGluSerIleGlyValMetGln 262
DB 742 TTATTGAAAGCAAGTATGTCGCGTACGTTTGAAGACAGATATCGAAACGATGAG 801
QY 263 GluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGlyPheVal 282
DB 802 GCTATGAACGTAGGAACGATGATTGAAGTTGTGTCAGGGGAAACATTAACCTGTTTGT 861
QY 283 LysValIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSerLeuValAla 302
DB 862 AAAAAAATTGACAAAACAATTTGAATGCAACCGTGTGGAAGATGTTGCAACATTAACAGAA 921
QY 303 LeuLeu 304
DB 922 ACGTTA 927
```

RESULT 11

US-10-282-122A-15949

Sequence 15949, Application US/10282122A

GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 15949

LENGTH: 927

TYPE: DNA

ORGANISM: Clostridium acetobutylicum

US-10-282-122A-15949

Alignment Scores:

Pred. No.: 1,69e-62 Length: 927
Score: 710.50 Matches: 146
Percent Similarity: 67.11% Conservative: 56
Best Local Similarity: 48.50% Mismatches: 96
Query Match: 46.81% Indels: 3
DB: 9 Gaps: 3

US-09-308-397-2 (1-306) x US-10-282-122A-15949 (1-927)

```
QY 3 LysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArgAspPhe 22
DB 7 AAGATTCGATTGTTTTCAGGACAGCGTTCGAGTATGTTGGATGGGAAGGATCTA 66
QY 23 TyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeuGlyTyr 42
DB 67 TACGATAATTACCAAGCGCAAGGAAACTTTTGATAAAGCTGATGAAGTGTCTGGCTTT 126
QY 43 AspLeuArgTyrLeu---IleAspThrGluAlaAspLysLeuAsnGlnThrArgTyrThr 61
DB 127 AAAATCAGTGAATATGCTTCGAGGAAAGATGAGAAATTAATTTAACTGAGACACT 186
QY 62 GlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeu---GlnGluLysGly 80
DB 187 CAGCCAGCAGTTTAACTACTAGTAGCTGCTTTAAGACACTTTAAGACACTTTGAAGAAAGAAAGGA 246
```

QY 81 TyrGlnProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaSer 100
Db 247 ATAAACCTGTATGTTGTCAGGTCTAAGCTTAGAGAGTATTCGCACATGTTGCAGT 306
QY 101 GlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyrMetGlu 120
Db 307 GGGAGTTTTCATTGAGGATCGAGTAAAGTATGTAAGGAGAGAGATATATGCAA 366
QY 121 GluAlaAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluVal 140
Db 367 GAAGCAGTACCAAAAGGAATAGGTACTATGCTCTCTAATCGGACTTGAAGGTGATGA 426
QY 141 IleGluGluAlaCysGlnLysAlaSerGluLeuGlyValValThrProAlaAsnTyrAsn 160
Db 427 GTTAGAGTATATGCGGTGACATCAAGAGAGATAGTAGAGGTAGCAATTAAT 486
QY 161 ThrProAlaGlnIleValIleAlaGlyGluValValAlaValAspArgAlaValGluLeu 180
Db 487 TGTCAGGACCAATTTGTTATAGCAGGAGAGTTAAAGCTGTTGAAGCGCTCTACTAAG 546
QY 181 LeuGlnGluAlaGlyAlaLysArgLeuIleProLeuLysValSerGlyProPheHisThr 200
Db 547 TTAAGGAACCGAGCAGAGAACAGTAAATGCTTTCAGTAAAGTGGACCATTTACACA 606
QY 201 AlaLeuLeuGluProAlaSerGlnLysLeuAlaGluThrLeuAlaGlnValSerPheSer 220
Db 607 TCTATGCTAAAGAGTGTCTGCTGAAAATTAAGAGCAATTAAGAGATATAATATAGAA 666
QY 221 AspPheThrCysProLeuValGlyAsn---ThrGluAlaValMetGlnLysGluAsp 239
Db 667 GATATGAGGTACCAAGTTTACAAATGTAAACAGAGACTATGTAGAAGATAAGGATCAG 726
QY 240 IleAlaGlnLeuThrArgGlnValLysGluProValArgPheTyrGluSerIleGly 259
Db 727 ATAAAGCTTTATTGAAAACCAAGTCATGAGCTCTGTAGATGGGAAGATACAATAAGA 786
QY 260 ValMetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSer 279
Db 787 AGAATGATGATGATGAGTATGAGTATACATTTATAGAGCTTGACCAAGTAAAGTAAAGT 846
QY 280 GlyPheValLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSer 299
Db 847 TCATTTATAAGAAATAATAGAAATAGCAATATATTAATTTGAAAAGCTGAGAT 906
QY 300 Leu 300
Db 907 TTA 909

RESULT 12
US-10-369-493-46809
; Sequence 46809, Application US/10369493
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 46809
; LENGTH: 954
; TYPE: DNA
; ORGANISM: Bacillus subtilis
US-10-369-493-46809

Alignment Scores: 2.62e-58 Length: 954
Pred. No.:

Score: 669.50 Matches: 143
Percent Similarity: 62.71% Conservative: 47
Best Local Similarity: 47.13% Mismatches: 110
Query Match: 44.10% Indels: 3
DB: 8 Gaps: 3
US-09-308-397-2 (1-306) x US-10-369-493-46809 (1-954)
QY 1 MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg 20
Db 1 ATGAGTAAGATTGCAATTTTATTCGCGGTTCAGGATCACAATTTATCGCATGGGAAAA 60
QY 21 AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeu 40
Db 61 GAGCTTTATGACAGTGCCTCTGCTGCCAAGCGTCTGTTGATGAGCGATGAACGTTG 120
QY 41 GlyTyrAspLeuArgTyrLeuIle---AspThrGluGluAspLysLeuAsnGlnThrArg 59
Db 121 GAAACAAAACCTCAGCTGCTTATTTTTCAGGGGATGCTGAAGAATTAACACTTACATAC 180
QY 60 TyrThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnGluLys 79
Db 181 AATGCGCAGCTGCTTTTTCAGCAAGCATCGCTGTTCTTGAGAAATTTAAGAAATCT 240
QY 80 GlyTyrGlnProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAla 99
Db 241 GGCATTACACCTGATTTCACAGCAGGACACAGCCTTGTGTAATTTCTGCACCTGGTTCG 300
QY 100 SerGlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyrMet 119
Db 301 GCTGCGCTGCTGCTTTCAAGATGCTGTTTATCTGTGAGAAAGCGCGGAGAGTTATG 360
QY 120 GluGluAlaAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGlu 139
Db 361 AATGAAGCGTCCGCTGCGGAGGAGCAATGGCTGCGATTCTTCGGCATGATGCTGAA 420
QY 140 ValIleGluGluAlaCysGlnLysAlaSerGluLeuGly---ValValThrProAlaAsn 158
Db 421 GCATTAAGCAAGTAACCGATAAAGTCACAGAGGAAGCAACCTTGTACAGCTGCGAAT 480
QY 159 TyrAsnThrProAlaGlnIleValIleAlaGlyGluValAlaValAlaValAspArgAlaVal 178
Db 481 CTCACCTGCTCGCCCAATTCGTATTTCGGAACAGCTAAAGGGGTTGACCTGCACT 540
QY 179 GluLeuLeuGlnGluAlaGlyAlaLysArgLeuIleProLeuLysValSerGlyProPhe 198
Db 541 GAACTGGCAAAAGAGACGCGCAAAACGCAATTCGCTTGAAGTAAAGCGGTCGCTTC 600
QY 199 HisThrAlaLeuGluProAlaSerGlnLysLeuAlaGluThrLeuAlaGlnValSer 218
Db 601 CATTCGAACTGATGAACCGCTGCTGAAAGCTGAAAGAGGTATTGGAGCGCTGTGAC 660
QY 219 PheSerAspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMet---GlnLys 237
Db 661 ATAAAAAGACGTCAGCTTCGCTCATCAATGTTCTGCTGACCTGATGACGTGAAAA 720
QY 238 GluAspIleAlaGlnLeuThrArgGlnValLysGluProValArgPheTyrGluSer 257
Db 721 GCAGATATCAAGAAAAAATTTATGAGCAGCTTTACTCTCCGGTTCGTTTGGAGAAAGC 780
QY 258 IleGlyValMetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysVal 277
Db 781 ATTAACAAGCTGATCGCAGAGGGTGTACGACTTTTATTGAATCGGTCCCGGAAAAAGTG 840
QY 278 LeuSerGlyPheValLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGln 297
Db 841 CTTTCAGCGCTTGTAAAAAAGTGAATAGACGGTTAAAAACAATTCGTGTATCATGATCCG 900
QY 298 AlaSerLeu 300
Db 901 GAAACGATC 909
RESULT 13

```

US-10-282-122A-41191
; Sequence 41191, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 41191
; TYPE: DNA
; ORGANISM: Vibrio cholerae
US-10-282-122A-41191

Alignment Scores:
Pred. No.:      Length:      4,298-57      939
Score:          657.50      Matches:      146
Percent Similarity: 66.23%      Conservative: 58
Best Local Similarity: 47.40%      Mismatches:  97
Query Match:      43.31%      Indels:       7
DB:                9        Gaps:         4

US-09-308-397-2 (1-306) x US-10-282-122A-41191 (1-939)
Qy      1 MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg 20
Db      16 ATGAGTAAAGTTTGCTATGCTATTTCCAGTCCAGGCTCGCAAGCAGTAGTATGCTGGCT 75
Qy      21 AppPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLys 40
Db      76 GACCTTGGCGAGCATGATGCTGTGTAAACAAACATTCGGCGAAGCTTCAGAAAGTGCTT 135
Qy      41 GlyTyrAspLeuArgTyrLeuIle---AspThrGluGluAspLysLeuAsnGlnThrArg 59
Db      136 GTTACGATCTCTGGCGCGTGTCTCAAGATGCGCCCTGTGGAAGATCTCAACCAACTTC 195
Qy      60 TyrThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuGlnGluLys 79
Db      196 CGTACTCAACCTGCGTGTGCTTCCCGCTCTGTTCGATTTGGCGTGTATGCGCAACACTG 255

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Qy      80 GlyTyr---GlnProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuVal 98
Db      256 GGTCTTGACCAACCTCGCGTTTACCTGCTACAGCTTGGGTGGATATTCACACTGGTA 315
Qy      99 AlaSerGlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyr 118
Db      316 TGTGGCGGCGTGTATTGATTTAAACAAGCATCAAGCTGGTTGAGCTGGTGGTCAATTG 375
Qy      119 MetGluGluAlaAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProVal 138
Db      376 ATGCAACAAGCGTGCCTCGCGTACGGGTCAATGTACCGCATCATGGTCTAGAAGAT 435
Qy      139 GluValIleGluGluAlaCysGlnLysAlaSerGluLeuGlyValValThrProAlaAsn 158
Db      436 GAAGCGATTGCTAAAGCTGTCTGACGCGGCGCAAGGTGAAGTGGTTTCTCTGTAAC 495
Qy      159 TyrAsnThrProAlaGlnIleValIleAlaGlyGluValValAlaValAspArgAlaVal 178
Db      496 TTAACTCAACGAGCGCAAGTGTATTGCTGTCTCAAAAAGATGCGGTTGAGCGTGGCG 555
Qy      179 GluLeuLeuGlnGluAlaGlyAlaLysArgLeuIleProLeuLysValSerGlyProPhe 198
Db      556 GTTCTGTGTAAAGACGCGGCGCAACGTCGCTGCGCTCTCCAGTTTCCGTACCATCA 615
Qy      199 HisThrAlaLeuGluProAlaSerGlnLysLeuAlaGluThrLeuAlaGlnValSer 218
Db      616 CACTGCGGCTTGATGAAGCTGCTGCGGATGAATGGCAAAACTCTAGCAGAGCTTGA 675
Qy      219 PheSerAspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGlu 238
Db      676 TTCATGTGCACCAAAATTCGGTCAATCAATAACGTTGAT-----GTTGGCTGAAACG 729
Qy      239 Asp-----IleAlaGlnLeuLeuThrArgGlnValLysGluProValArgPheTyr 255
Db      730 GATCCGGTAAATTAAGCATGGTGTATGCTCAACTCTATAGCCAGTTCGTTGGACT 789
Qy      256 GluSerIleGlyValMetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyProGly 275
Db      790 GAATGGGTTGAACAAATGAGCGCACAAAGGTGCGAAAGCTGATTGAAATGGGCGCGGT 849
Qy      276 LysValLeuSerGlyPheValLysLysIleAspGlnThrAlaHisLeuAlaHisValGlu 295
Db      850 AAGTATTGACTGCTTAACAAACGTTATTGTAAAAACCTTAGAAGGTGTCGACGTCAT 909
Qy      296 AspGlnAlaSerLeuValAlaLeu 303
Db      910 GACGTGCTCTTTGGATGCGGTG 933

```

RESULT 14

```

US-10-369-493-41012
; Sequence 41012, Application US/10369493
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianning
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 41012
; LENGTH: 942
; TYPE: DNA
; ORGANISM: Bacillus halodurans
US-10-369-493-41012
Alignment Scores:

```

Pred. No.: 9,78e-57 Length: 942
Score: 654.00 Matches: 141
Percent Similarity: 64.40% Conservative: 58
Best Local Similarity: 45.63% Mismatches: 106
Query Match: 43.08% Indels: 4
DB: 8 Gaps: 4

US-09-308-397-2 (1-306) x US-10-369-493-41012 (1-942)

QY 1 MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg 20
DB 1 ATGGCAAAAGTAGATTTCTATTCCAGGTCAGGCTCACAGTCTGTCGGCATGGGAGC 60
QY 21 AspPheTyrAspGlnTyrProIleValIysGluThrIleAspArgAlaSerGlnValLeu 40
DB 61 GAATTACTTTCAGAGGAAAA---GCAAAAGAGATTTTTCAGAGGCGGATGAAGACTC 117
QY 41 GlyTyrAspLeu---ArgTyrLeuIleAspThrGluGluAspLysLeuAsnGlnThrArg 59
DB 118 GCCTATTCCTTTCAGCATTTATGTTGAGCGGCGAGAAATAATTCGCCGCGAGCGAA 177
QY 60 TyrThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnGluLys 79
DB 178 AATACGCAACCGGCTTTCAGCATGAGCAGCGCGCTTTATCGCTCGTGGTGAATAT 237
QY 80 GlyTyrGlnProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAla 99
DB 238 GGAATCAACCTGATATACAGCGGCTCATAGTTAGGGAGTACAGTCCCTTGTGGCT 297
QY 100 SerGlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyrMet 119
DB 298 TCAGGCTCTTAACGTTTGGCGAGTGTGTGACGCTGTCATCCCGTTCATCCCGTGTATG 357
QY 120 GluGluAlaAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGlu 139
DB 358 GAAGAAGCGGTACATTCGGCGAAGGAGCAATGCGTCCATCTTGGCATGGAGCGGAC 417
QY 140 ValIleGluGluAlaCysGlnLysAlaSerGluLeuGly---ValValThrProAlaAsn 158
DB 418 GAATTAGAACAAAGTAACAGCGGCTAACAGACGAGGGGTGCTGTTGAATTCGAAC 477
QY 159 TyrAsnThrProAlaGlnIleValIleAlaGlyGluValValAlaValAspArgAlaVal 178
DB 478 TTAACACTGCTCGGCAAAATGTATCTCAGGTTCTGCTGAGGCTGTCGACACAGCATCA 537
QY 179 GluLeuLeuGlnGluAlaGlyAlaLysArgLeuIleProLeuLysValSerGlyProPhe 198
DB 538 GAGGAAGCAAGAGAGCAGGCGGAGGAGTATCCCATTTGCAAGTGCAGCGACCGTTT 597
QY 199 HisThrAlaLeuLeuGluProAlaSerGlnLysLeuAlaGluThrLeuAlaGlnValSer 218
DB 598 CATTTCATCGCTTATGAAACCGGCTGCCGAAAGCTTGAAGCGGTGTTAGCGCATTTGCA 657
QY 219 PheSerAspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLys--- 237
DB 658 ATCGCTGATGCGCTCCACCTGTTATTCCTCAATGTGACAGCATCTGCTCAAAAGCC 717
QY 238 GluAspIleAlaGlnLeuLeuThrArgGlnValLysGluProValArgPheTyrGluSer 257
DB 718 GCTGACATTCGCTCATCTCTATTGAGCAAGTACTCTCCAGTTCGTTGGAGGACACT 777
QY 258 IleGlyValMetGlnGluAlaGlyIleSerAsnPheIleGlyProGlyLysVal 277
DB 778 GTTCGTCGATCTTACTGCTGAGTGGATACGTTGCGGAAATTCGGATCAGGAATGTG 837
QY 278 LeuSerGlyPheValLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGln 297
DB 838 CTCTCAGGCTCTGTCGCAAAAGTACAGGCGCGGTTAATGTTTTCTGTGAGTGATCGG 897
QY 298 AlaSerLeuValAlaLeuLeuGluLys 306
DB 898 GCAGCATTTGAAGCGCATGTTAAAAA 924

RESULT 15
US-10-282-122A-32186
; Sequence 32186, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carz, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32186
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-10-282-122A-32186

Alignment Scores:
Pred. No.: 2,76e-56 Length: 930
Score: 649.50 Matches: 145
Percent Similarity: 63.84% Conservative: 51
Best Local Similarity: 47.23% Mismatches: 108
Query Match: 42.73% Indels: 3
DB: 9 Gaps: 3

US-09-308-397-2 (1-306) x US-10-282-122A-32186 (1-930)

QY 1 MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg 20
DB 1 ATGACTGATTTTGCAATGGTTTCCCTGACAGGATCACAGCGATGGAATGCTTGA 60
QY 21 AspPheTyrAspGlnTyrProIleValIysGluThrIleAspArgAlaSerGlnValLeu 40
DB 61 GAATTCGCGCATTTATCCATAGTAGTACAGAAACATTTGCTCAAGCATCTGATGTTG 120
QY 41 GlyTyrAspLeuArgTyrLeuIleAspThr---GluGluAspLysLeuAsnGlnThrArg 59
DB 121 GGTATTCTCTTGGGATTTAGTGCAAAATGCTCTGAGAGAGAGTTAAACAACATGG 180
QY 60 TyrThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnGluLys 79

Db 181 AAAACACAGCGGCATTATTAGCAGCATCCGTTGCTATTGGCGAGTATGGCAAGAAAA 240
 QY 80 ---GlyTyrGlnProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuVal 98
 Db 241 CAAGGCAAAATGCCAAATGATGGCAGGTACAGCTTTGGTGAGTATTCCTTTAGTC 300
 QY 99 AlaSerGlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyr 118
 Db 301 TGTGCTGGGGTAATTGATTTGCTGGGGGATTAACTAGTAGAATTGGCGGTCAATTA 360
 QY 119 MetGluGluAlaAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProVal 138
 Db 361 ATGCAAGAGCGCTGTACTCGAGTACTGGCGCATGTATGCAATTATCGGATTAGATAAT 420
 QY 139 GluValIleGluGluAlaCysGlnLysAlaSerGluLeuGlyValValThrProAlaAsn 158
 Db 421 GATGCTATTGCCAAAGCTTGTGNAGATGGGGTCAAGGACAAGTTGTCTCACCCTGTGAAC 480
 QY 159 TyrAsnThrProAlaGlnIleValIleAlaGlyGluValAlaValAlaAspArgAlaVal 178
 Db 481 TTTAACTCACCGGTCAAGTGGTGAATTGGCGGTAAATAAAGAACCGGTAGAGCGTGCAGGG 540
 QY 179 GluLeuLeuGlnGluAlaGlyAlaLysArgLeuIleProLeuLysValSerGlyProPhe 198
 Db 541 GCATTATGTAAAGAGCTGGAGCGAAACGTGGCTTACCTTTAGCGTAAGTGTGCTTCT 600
 QY 199 HisThrAlaLeuLeuGluProAlaSerGlnLysLeuAlaGluThrLeuAlaGlnValSer 218
 Db 601 CACTGTGCTTTAATGAAGCTGCTGCAGATAAGTTAGCTGTTGCATTGCAAGAAATTGAA 660
 QY 219 PheSerAspPheThrCysProLeuValGlyAsnThrGluAla--AlaValMetGlnLys 237
 Db 661 TTTAAACACCTGAAATTCAGTTGTTAATATGTTGTAAGTGAAGCAACACCGATGCT 720
 QY 238 GluAspIleAlaGlnLeuLeuThrArgGlnValLysGluProValArgPheTyrGluSer 257
 Db 721 AATGCTATTGAGATGCATTAGTTGCTCAGCTTTATACCCAGTCCGCTGGACTGAAACG 780
 QY 258 IleGlyValMetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysVal 277
 Db 781 GTTGAATTTATTGCTGTAAGGGCATCACACAATTATTAGAATAGGACCCGCTAAAGTA 840
 QY 278 LeuSerGlyPheValLysLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGln 297
 Db 841 TTTACTGGTTTAAAGCAACGCTATTCTTAAGAGATGACGCTGCAGCAGTTAATGATATT 900
 QY 298 AlaSerLeuValAlaLeuLeu 304
 Db 901 GCATCATTAGACGCTGCATTA 921

Search completed: June 11, 2003, 22:14:11
 Job time : 671 secs